

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2003, 09:50:12 : Search time 23 Seconds
(Without alignments)

2119,892 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671

Sequence: 1 MAGRSLVSWRAFGCDSEAE.....PASVSGDADGSTRSPRQEP 507

Scoring table: BIOSUM62

Gapop 10.0 , Gapect 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2671	100.0	507	2	A55625 protein-tyrosine k
2	2445	91.5	527	2	A49865 protein-tyrosine k
3	2341	87.6	505	2	I59296 protein-tyrosine k
4	2221.5	83.2	467	2	I56579 protein-tyrosine k
5	2209.5	82.7	465	2	I48926 protein-tyrosine k
6	1253.5	46.9	450	2	I41973 protein-tyrosine k
7	1245.5	46.6	450	1	JH0559 protein-tyrosine k
8	1242.5	46.5	450	1	S15094 protein-tyrosine k
9	1227.5	46.0	450	2	I48929 protein-tyrosine k
10	762.5	28.5	507	1	A39939 protein-tyrosine k
11	751.5	28.1	509	1	I48845 protein-tyrosine k
12	742.5	27.8	509	1	OKH0LK protein-tyrosine k
13	736	27.6	545	2	S52313 protein-tyrosine k
14	735	27.5	533	1	TVCHS protein-tyrosine k
15	734.5	27.5	526	1	TVFV60 protein-tyrosine k
16	734.5	27.5	568	1	TVFV51 protein-tyrosine k
17	734	27.5	557	1	TVFV52 protein-tyrosine k
18	733	27.4	546	2	S52314 protein-tyrosine k
19	731.5	27.4	587	1	TVFVPR protein-tyrosine k
20	730.5	27.3	526	2	S20808 protein-tyrosine k
21	730.5	27.3	526	2	S26420 protein-tyrosine k
22	727.5	27.2	523	1	TVFVMT protein-tyrosine k
23	724.5	27.1	526	1	OKFVYR protein-tyrosine k
24	724	27.1	532	1	A34104 protein-tyrosine k
25	724	27.1	532	1	A34104 protein-tyrosine k
26	724	27.1	1520	1	TVFVFA protein-tyrosine k
27	723.5	27.1	526	1	TVFVFA protein-tyrosine k
28	720.5	27.0	505	1	TVH0UC protein-tyrosine k
29	718	26.9	542	1	TVH0UC protein-tyrosine k

30	716.5	26.8	526	2	S15582 protein-tyrosine k
31	716	26.8	505	1	S24550 protein-tyrosine k
32	714	26.7	541	1	A43610 protein-tyrosine k
33	713	26.7	506	1	S24553 protein-tyrosine k
34	713	26.7	512	1	I56160 protein-tyrosine k
35	713	26.7	528	1	TVFVCG protein-tyrosine k
36	710	26.6	541	2	S31645 protein-tyrosine k
37	710	26.6	543	1	TVH0VS protein-tyrosine k
38	709	26.5	537	2	I51592 protein-tyrosine k
39	707	26.5	512	1	TVH0LK protein-tyrosine k
40	706	26.4	541	1	TVCHRS protein-tyrosine k
41	706	26.4	542	2	A49114 protein-tyrosine k
42	705	26.4	544	2	I51593 protein-tyrosine k
43	701	26.2	512	1	A39719 protein-tyrosine k
44	700.5	26.2	503	1	J01371 protein-tyrosine k
45	699.5	26.2	536	2	S33569 protein-tyrosine k

ALIGNMENTS

RESULT 1

protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
A:Accession: A55625
N:Alternate names: hematopoietic consensus tyrosine-lacking (HYL) non-receptor tyrosi
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1995 #sequence, revision 24-Feb-1995 #text, change 26-May-2000
C:Accession: A55625; S43533; I58397; T46523
J:Avraham, S.; Jiang, S.; Oka, S.; Fu, Y.; Deng, B.; Dowler, L.L.; White, R.A.; Avrah
J. Biol. Chem. 270, 1833-1842, 1995
A:Title: Structural and functional studies of the intracellular tyrosine kinase MATK
A:Reference number: A55625; MUID:95130565; PMID:7530249
A:Accession: A55625
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-507 <AVR>
A:Cross-references: GB:S75164; NID:9896217; PIDN:MAC60645.1; PID:9896220
R:Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.; Suda, T.
Oncogene 9, 1155-1161, 1994
A:Title: Molecular cloning of a novel non-receptor tyrosine kinase, HYL (hematopoietic
A:Reference number: I58397; MUID:94268844; PMID:7516063
A:Accession: I58397
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 42-149, 'GG', 152-160, 'T', 162-258, 'C', 261-296, 'D', 298-336, 'R', 338-362, 'E', 3
A:Cross-references: GB:S71669; NID:9559593; PIDN:AA30995.1; PID:9559594
R:Duesterhoft, A.; Lauber, J.; Mewes, H.W.; Well, B.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23036
A:Accession: T46323
A:Molecule type: mRNA
A:Residues: 'GNGATRSKSLGVRSLAELGAGAGSGAPPEQ', 25-507 <AAA>
A:Cross-references: EMBL:AL137754
C:Experimental source: adult testis; clone DKFZp434N1212
C:Comment: For an alternative splice form, see PIR:A4965.
C:Genetics:
A:Gene: GDB:MATK; lsk
A:Cross-references: GDB:304667
A:Map position: 19p13.3-19p13.3
A:Note: DKFZp434N1212.1
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
C:Keywords: alternative splicing; ATP; phosphotransferase; tyrosine-specific protein
F:55-105/Domain: SH3 homology <SH3>
F:122-211/Domain: SH2 homology <SH2>

F:233-485/Domain: protein kinase homology <KIN>
F:241-249/Region: protein kinase ATP-binding motif

Query Match 100.0%; Score 2671; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 4.5e-130;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAGRGLSVRAHFGCDASAEELPRVSPRFLRAWHPPVSAARMPTRRAPPTQCTTCENT 60
DB 1 MAGRGLSVRAHFGCDASAEELPRVSPRFLRAWHPPVSAARMPTRRAPPTQCTTCENT 60
QY 61 RPRPGLAIFRKGDVVTLLKCEKNSWYRVKHHHTSGOGLLAAGALRREALSDPKLSLM 120
DB 61 RPRPGLAIFRKGDVVTLLKCEKNSWYRVKHHHTSGOGLLAAGALRREALSDPKLSLM 120
QY 121 PMFHGKISGGEAVOQLOPPEDGLFLVRESARHPGDVYLCSFGRDVYHRYVLRHDLTI 180
DB 121 PMFHGKISGGEAVOQLOPPEDGLFLVRESARHPGDVYLCSFGRDVYHRYVLRHDLTI 180
QY 181 DEAVFPCNLDMDVNEHYSKDKGALCTKLVRPKRKHGTSABEELARAGWMLNLOHLLGAQ 240
DB 181 DEAVFPCNLDMDVNEHYSKDKGALCTKLVRPKRKHGTSABEELARAGWMLNLOHLLGAQ 240
QY 241 IGGEGEAVLQGEYLGOKVAVKNIKCDVTAQAFLEDAVMTKMHENLVRLGLVILHOGI 300
DB 241 IGGEGEAVLQGEYLGOKVAVKNIKCDVTAQAFLEDAVMTKMHENLVRLGLVILHOGI 300
QY 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKLVRHDLAARNILV 360
DB 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKLVRHDLAARNILV 360
QY 361 SEDLVAKVSPFGAKAKRKLDSSRLPVKWTAPALKHGFSTKSDVMSGVLLMEVFSY 420
DB 361 SEDLVAKVSPFGAKAKRKLDSSRLPVKWTAPALKHGFSTKSDVMSGVLLMEVFSY 420
QY 421 GRAPYPRMSLKEYSEAVEKEGYRMEPEGCGPVHVLMSQWEAPARPPFRKLAEKLAR 480
DB 421 GRAPYPRMSLKEYSEAVEKEGYRMEPEGCGPVHVLMSQWEAPARPPFRKLAEKLAR 480
QY 481 ELRSAGAPASVSGODADGSTSPRSQEP 507
DB 481 ELRSAGAPASVSGODADGSTSPRSQEP 507

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RESULT 2

A:Accession: A49865
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-527 <BEN>
A:Cross-references: GB:L18974; NID:9455449; PIDN:AAA16703.1; PID:94559550
C:Comment: For an alternative splice form, see PIR:A55625.
C:Genetics:
A:Gene: GDB:MATK.1sk
A:Cross-references: GDB:304667
A:Map position: 19p13.3-19p13.3
A:Note: DKFZP434N1212.1
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology; SH3 domain; SH3 homology <SH3>
F:122-211/Domain: SH2 homology <SH2>
F:233-484/Domain: protein kinase homology <KIN>
F:241-249/Region: protein kinase ATP-binding motif

Query Match 91.5%; Score 2445; DB 2; Length 527;
Best Local Similarity 93.5%; Pred. No. 1.8e-118;
Matches 472; Conservative 1; Mismatches 18; Indels 14; Gaps 2;

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QY 1 MAGRGLSVRAHFGCDASAEELPRVSPRFLRAWHPPVSAARMPTRRAPPTQCTTCENT 60
DB 1 MAGRGLSVRAHFGCDASAEELPRVSPRFLRAWHPPVSAARMPTRRAPPTQCTTCENT 60
QY 61 RPRPGLAIFRKGDVVTLLKCEKNSWYRVKHHHTSGOGLLAAGALRREALSDPKLSLM 120
DB 61 RPRPGLAIFRKGDVVTLLKCEKNSWYRVKHHHTSGOGLLAAGALRREALSDPKLSLM 120
QY 121 PMFHGKISGGEAVOQLOPPEDGLFLVRESARHPGDVYLCSFGRDVYHRYVLRHDLTI 180
DB 121 PMFHGKISGGEAVOQLOPPEDGLFLVRESARHPGDVYLCSFGRDVYHRYVLRHDLTI 180
QY 181 DEAVFPCNLDMDVNEHYSKDKGALCTKLVRPKRKHGTSABEELARAGWMLNLOHLLGAQ 240
DB 181 DEAVFPCNLDMDVNEHYSKDKGALCTKLVRPKRKHGTSABEELARAGWMLNLOHLLGAQ 240
QY 241 IGGEGEAVLQGEYLGOKVAVKNIKCDVTAQAFLEDAVMTKMHENLVRLGLVILHOGI 300
DB 241 IGGEGEAVLQGEYLGOKVAVKNIKCDVTAQAFLEDAVMTKMHENLVRLGLVILHOGI 300
QY 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKLVRHDLAARNILV 360
DB 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKLVRHDLAARNILV 360
QY 361 SEDLVAKVSPFGAKAKRKLDSSRLPVKWTAPALKHGFSTKSDVMSGVLLMEVFSY 420
DB 361 SEDLVAKVSPFGAKAKRKLDSSRLPVKWTAPALKHGFSTKSDVMSGVLLMEVFSY 419
QY 421 GRAPYPRMSLKEYSEAVEKEGYRMEPEGCGPVHVLMSQWEAPARPPFRKLAEKLAR 480
DB 421 GRAPYPRMSLKEYSEAVEKEGYRMEPEGCGPVHVLMSQWEAPARPPFRKLAEKLAR 479
QY 481 ELRSAGAPASVSGODADGSTSPRSQ. 505
DB 470 ---SAMPYPRMSLKEYSEAVEKEGYRMEPEGCGPVHVLMSQWEAPARPPFRKLAEKLAR 491

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RESULT 3

A:Accession: I59296
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-505 <RES>
A:Cross-references: GB:L27738; NID:9507289; PIDN:AAB59677.1; PID:9507290
R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, Oncogene 9, 3437-3448, 1994
A:Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine pro
A:Reference number: I58407; MUID:95060800; PMID:7970703
A:Accession: I58407
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-43 <RE2>
A:Cross-references: GB:I33339; NID:9609536; PIDN:AAA64431.1; PID:9609537
R:Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler, L.L.; White, R.A.; Avrah
J. Biol. Chem. 270, 1833-1842, 1995
A:Title: Structural and functional studies of the intracellular tyrosine kinase MATK
A:Reference number: A55625; MUID:95130565; PMID:7530249
A:Accession: B55625
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 41-505 <AVR>
R:Keneko, Y.: Nomoguchi, K.: Fukuyama, H.: Takano, S.: Hishanitsuji, H.: Nishiyama, H.:
Oncogene 10, 945-952, 1995
A:Title: Presence of alternative 5' untranslated sequences and identification of cells e
A:Reference number: 149621; MUID:95206787; PMID:7898936
A:Accession: I49621
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 41-505 <RE3>
A:Cross-references: GB:D45243; NID:g659858; PIDN:BAA08199.1; PID:g659859
C:Genetics:
A:Gene: Ntk; p56nTk
A:Introns: 23/3
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:53-103/Domain: SH3 homology <SH3>
F:120-209/Domain: SH2 homology <SH2>
F:231-483/Domain: protein kinase homology <KIN>
F:239-247/Region: protein kinase ATP-binding motif

Query Match	87.6%;	Score 2341;	DB 2;	length 505;
Best Local Similarity	87.4%;	Pred. No. 3.7e-113;		
Matches 443; Conservative	27;	Mismatches 35;	Indels 2;	Gaps 2

QY	1	MAGGSLVSRBAFFGCDSSAEELPRVSPRLFRAMHPVYSAMPYRMRNAQCSTKCEHT	60
Db	1	MASSSVSMIALEFGMES - RDLPRVSPRLGAMHHPAAAAARMP - RRAFGQCTKCEHS	58
QY	61	RPRGEBELAFRKGDVYVTLLEACENKSWYRVKHHHSGOGLLAAGALREREALSADPKLSLM	120
Db	59	RPRGEBELAFRKGDVYVTLLEACEDKSWYRAKHGSGOGLLAALALROREALSTDPKLSLM	118
QY	121	PMFNGKISGQEAVOQLORPEDGLFLYRESARHPDDYVLVCSFGADYVHYRVLHSDGHLTI	180
Db	119	PMFNGKISGQEAIOQLORPEDGLFLYRESARHPDDYVLVCSFGADYVHYRVLHSDGHLTI	178
QY	181	DEAVFPCNLMDMVEHYSKDKGAICTKLVPRKRKHGTSAEBELARAGMLNLQHLTLGAQ	240
Db	179	DEAVCFPCNLMDMVEHYTKDKGALICTKLVPRKKGASAEBELAKAGMLDLQHLTLGAQ	238
QY	241	IGSECFGAVLOGEVLGQKVAVKNIKCDVTQOAFIDETRAVYMKMHNLVRLGLYTLGQGL	300
Db	239	IGSECFGAVLOGEVLGQKVAVKNIKCDVTQOAFIDETRAVYMKLQVRLHNLVRLGLYTLHNGL	298
QY	301	YIVMEHYSKGNLVNFLTGRBALVNTAQLDQFSLHVAEGMEYLESKKLVHRDLAARNILY	360
Db	299	YIVMEHYSKGNLVNFLTGRBALVNTAQLDQFSLHVAEGMEYLESKKLVHRDLAARNILY	358
QY	361	SEDIYVAVSPGGLAKAARRKGLDSSRLPYKMTAPALAHGKTSSDVMWSRGVLLMVEFSY	420
Db	359	SEDIYVAVSPGGLAKAARRKGLDSSRLPYKMTAPALAHGKTSSDVMWSRGVLLMVEFSY	418
QY	421	GRAYPMSLSKEVSEAVEKGYRMEPPGCGCPYVHVLMSGCWEAPARPARPPEKRLAEKTLAR	480
Db	419	GRAYPMSLSKEVSEAVEKGYRMEPPGCGCPYVHVLMSGCWEAPARPARPPEKRLAEKTLAR	478
QY	481	ELRSAGAPASVSGDADGCTSPRSQEP	507
Db	479	ELRSVGSAPRGQEAEGSAPTRSQEP	505

RESULT 4
I56579
Protein-tyrosine kinase (EC 2.7.1.112) batk - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 04-Mar-2000
C:Accession: I56579
R:Kuo, S.S.; Moran, P.; Gripp, J.; Armanini, M.; Phillips, H.S.; Goddard, A.; Caras, I., V.
J. Neurosci. Res. 38, 705-715, 1994
A:Title: identification and characterization of Batk, a predominantly brain-specific non-
A:Reference number: I56579; MIMD:95106341; PMID:7807586
A:Accession: I56579
A:Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: DNA
A: Residues: 1-467 <RES>
A: Cross-references: GB:U34542; NID:g530157; PIDN:AAA64524.1; PID:g530158
C: Genetics:
A: Gene: batk
C: Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
C: Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F: 14-64/Domain: SH3 homology <SH3>
F: 81-170/Domain: SH2 homology <SH2>
F: 193-445/Domain: protein kinase homology <KIN>
F: 200-208/Region: protein kinase ATP-binding motif

Query Match	83.2%;	Score 2221.5;	DB 2;	Length 467;
Best Local Similarity	89.3%;	Pred. No. 4.5e-107;		
Matches 417;	Conservative 27;	Mismatches 22;	Indels 1;	Gaps 1

[illegible]

RESULT 5
 148926
 protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse
 Alternate names: csk-type protein-tyrosine kinase
 Species: Mus musculus (house mouse)
 Date: 15-Mar-1996
 Accession: 148926
 Update: 148926
 Klages, S.; Adam, D.; Class, K.; Fargnoli, J.;
 Proc Natl. Acad. Sci. U.S.A. 91, 2597-2601, 1994
 Title: Ctk: a protein-tyrosine kinase related to Csk that defines an enzyme family.
 Reference number: A53469; MUID:94195789; PMID:7511815
 Accession: 148926
 Status: preliminary
 Molecule type: mRNA
 Residues: 1-465 <RES>
 Cross-References: EMBL:U05210; NID:q450232; PIDD:AA18829.1; PID:q450233
 Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3
 Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
 13-63/Domain: SH3 homology <SH3>
 80-169/Domain: SH2 homology <SH2>
 191-443/Domain: protein kinase homology <KIN>
 199-207/Region: protein kinase ATP-binding motif

[illegible]

Query Match	Best Local Similarity	Matches 234; Conservative	46.9%; Score 1253.5; DB 2; Length 450; Pred. No. 1.8e-57; Mismatches 113; Indels 3; Gaps 2;
47	WAPGTCQITRCCEHPRKPKGLAFKRGDVTILEACEKSWRYKHHRTSGOGLAAGLR	106	
Db	8 WPSSTECIAKTNHFGTAEQDLFPKSGDVLITVATKTPNNYKAKNKY-GREGIIPANYVQ	66	
107	EREALSDPKLISLMPWFHGRKISQGEAVQLOPPEDGLFLVRESARHDPDYVLCSFGSDV	166	
Db	67 KREGVYKAGIKLISLMPWFHGRKTKTREQAERLLYPETGLFLVRESSTNYGDTILVCSCEGV	126	
167	IHYVYLRDGHLLTIDEAVFNCNLMQVNEHYSKDGALICTLVLRPKRHGKRSABEELARA	226	

Db	127	EHRRIIYSSSKSLIDEVEYFENLMQVJEHYTTDDAGDGLCSRLIKRKWMEGVAAODESRS	186
OY	227	GWLNTQHLTLGAQIGEGFEAGVLOGEYLGOKVAAKNIKCDVYTAQALDELTAHYTKMOHE	286
Db	187	GMAIANKDKLQIITIGKIGEGCVMLGADYRGKVAVKCKIKNDATAOALAEASVYTOILRHS	246
OY	287	NLVRLLGVLLHQ--GLYLVMEHVS KGNLVNFLTFRGALVYTAOLLOFSLVHAEGMEYLE	344
Db	247	NLVQLLGVLYVEEKSGLYITTEYMAANGSLVYDLRSRGRSVLGGDCLLFKSIDVCEAMYLE	306
OY	345	SKTLVHRDLAARILVSEDLVAKVSDGCLAAERKGLDSSLPYKMYAPALAKHGRFTSK	404
Db	307	ANNFVHRDLAARVLSVSDNIAKVSADPGLTCEASTDTGTGLPKMYAPALAEKREKFEISK	366
OY	405	SDVMSFGLVLLMEVFSYGRAPYPRKMSLKEVSEAEVKEGKYMREPPGCGPVHYLMSCEAE	464
Db	367	SDVMSFGLIIMLEWFSYGRVYPRILPKDVPEVEKGYKMDPPDCPAIYEVNKKCWTLTD	426
OY	465	PARRPEPRKLAETL 478	
Db	427	PGHRPFSHQLEQL 440	

RESULT 7
 JH0559
 protein-tyrosine kinase (EC 2.7.1.112) CSK - human
 N:Alternate names: protein-tyrosine kinase cpl; protein-tyrosine kinase T2
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence, revision 20-Aug-1994 #text_change 21-Jul-2000
 C:Accession: JH0559; S38818; S19024; S19025
 R:Brauninger, A.; Holtrich, U.; Streibhardt, K.; Ruebsamen-Walggmann, H.
 Gene 110, 205-211, 1992
 A:Title: Isolation and characterization of a human gene that encodes a new subclass O
 A:Reference number: JH0559; MUID:92165060; PMID:11371469
 A:Accession: JH0559
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-450

 A:Cross-references: EMBL:X59932; NID:g30255; PIDN:CAA42556.1; PID:g30256
 R:Experimental source: Lung
 R:Brauninger, A.; Kern, T.; Streibhardt, K.; Ruebsamen-Walggmann, H.
 Oncogene 8, 1365-1369, 1993
 A:Title: Characterization of the human CSK locus.
 A:Reference number: S38818; MUID:93241739; PMID:7683131
 A:Accession: S38818
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-450

 A:Cross-references: EMBL:X74765; NID:g402582; PIDN:CAB58562.1; PID:g6077093
 R:Patlauer, J.; Armstrong, E.; Bergman, M.; Maekelae, T.P.; Hironen, H.; Huebner, K.
 Oncogene 6, 2013-2018, 1991
 A:Title: cpl encodes a putative cytoplasmic tyrosine kinase lacking the conserved tyr
 A:Reference number: S19024; MUID:92050797; PMID:11945408
 A:Accession: S19024
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-450 <PAR>
 A:Cross-references: EMBL:X60114; NID:g30314; PIDN:CAA42713.1; PID:g30315
 R:Holtrich, U.; Brauninger, A.; Streibhardt, K.; Ruebsamen-Walggmann, H.
 Proc. Natl. Acad. Sci. U.S.A. 88, 10411-10415, 1991
 A:Title: Two additional protein-tyrosine kinases expressed in human lung: fourth memb
 A:Reference number: S19025; MUID:92073297; PMID:11720539
 A:Accession: S19025
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-450 <HOL>
 A:Cross-references: EMBL:X59932; NID:g30255; PIDN:CAA42556.1; PID:g30256
 A:Note: This sequence was submitted to the EMBL Data Library, June 1991
 C:Comment: This protein lacks the N-myristylation and autophosphorylation sites prese
 C:Genetics:
 A:Gene: GDB:CSK
 A:Cross-references: GDB:131642; OMIM:124095
 A:Map position: 15q23-15q25
 A:Introns: 5/3; 43/3; 81/2; 154/3; 186/1; 208/1; 241/2; 271/3; 296/2; 361/3; 390/3

protein-tyrosine kinase (EC 2.7.1.112) CSK - rat
N.Alternate names: c-src kinase; tyro-13 kinase
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 11-Jun-1999
C.Accession: S15094; #sequence_revision 30-Jun-1993
R.Nada, S.; Okada, M.; MacAuley, A.; Cooper, J.A.; Nakagawa, H.
Nature 351, 69-72, 1991
A.Title: Cloning of a complementary DNA for a protein-tyrosine kinase that specifically
A.Reference number: S15094; MUID:91226538; PMID:1709258
A.Accession: S15094
A.Molecule type: mRNA
A.Residues: 1-450 <NAD1>
A.Cross-references: EMBL:X58631; NID:g57507; PIDN:CAA41484.1; PID:g57508
A.Accession: S18500
A.Molecule type: protein
A.Residues: 44-49; 54-67; 77-86; 126-137; 330-337; 352-360; 367-376; 394-401 <NAD>
R.Lal, C.; Lemke, G.
Neuron 6, 691-704, 1991
A.Title: An extended family of protein-tyrosine kinase genes differentially expressed in
A.Reference number: PT0183; MUID:91222560; PMID:2025425
A.Accession: PT0195
A.Molecule type: mRNA
A.Residues: 319-367 <LAT>
A.Experimental source: sciatic nerve

protein-tyrosine kinase (EC 2.7.1.112) Csk - mouse
M.Alternate names: protein-tyrosine kinase Mpk-2
C.Species: Mus musculus (house mouse)
C.Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 18-Feb-2000
C.Accession: I48929; S30498
R.Klages, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J.B.; Penhallow, R.C.
Proc. Natl. Acad. Sci. U.S.A., 91, 2597-2601, 1994
A.Title: Csk: a protein-tyrosine kinase related to Csk that defines an enzyme family
A.Reference number: A53469; MUID:94195789; PMID:7511815
A.Accession: I48929
A.Molecule type: mRNA
A.Residues: 1-450 <RES>
A.Cross-references: EMBL:U05247; NID:9452471; PIDN:AAAI8766.1; PID:9452472
R.Gillard-Hohenstelt, P.; Nieto, M.A.; Frahn, M.; Mattei, M.G.; Chestler, A.; Walk
Oncogene 7, 2499-2506, 1992
A.Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed
A.Reference number: S30496; MUID:93096484; PMID:1281307
A.Accession: S30498
A.Molecule type: mRNA
A.Residues: 316-367 <IIL>
A.Cross-references: EMBL:X57242; NID:953189; PIDN:CAA40518.1; PID:953190
C.Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
C.Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F.16-65/Domain: SH homology <SH3>

R:Garvin, A.M.; Pawar, S.; March, J.D.; Perlmutter, R.M.
 Mol. Cell. Biol. 8, 3058-3064, 1988
 A:Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell
 A:Reference number: 157636; MUID:89096891; PMID:2850479
 A:Accession: 177452
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-35, 'VR' <GRR>
 A:Cross-references: GB:M2151; NID:g198768; PIDN:AAA39422.1; PID:g554186
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3
 C:Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
 F:68-116/Domain: SH3 homology <SH3>
 F:127-224/Domain: SH2 homology <SH2>
 F:243-501/Domain: protein kinase homology <KIN>
 F:251-259/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:273/Active site: lvs #status predicted
 F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 28.1%; Score 751.5; DB 1; Length 509;
 Best Local Similarity 38.3%; Pred. No. 1,1e-31;
 Matches 164; Conservative 84; Mismatches 155; Indels 25; Gaps 9;
 Oy 65 GELAFRRGDVVTILEACENKSWYRKHTSGQEGILAAAGLREREALSADPKLSIMPFH 124
 Db 78 GDLFEKGEOLRIE--QSGEMKAOGLTGGEGFIDFNFAKANSLEPE-----PMWF 129
 Oy 125 GKIGQAVQOOLDPED--GLFLVRESARHAGDYLVY-----SFGRDVHYRYLHND-G 176
 Db 130 KNLSRKAERQLAPGHTHSEFLRESESTAGSFLVRPDQNGEVVKKYKTRNDNG 189
 Oy 177 HLTFDEAVFCNLMDNVEHYSKDKAICTLVPRKRGKTSAREEELARAGMLNLQHLT 236
 Db 190 GFYISPRITPGRCHLDVLRHTNMSDGLCTKLSRQC---IQPKPKMMEDEMEPRERIK 246
 Oy 237 LGAGIIGSEFGAVLQGEYLGO-KVAVKNIK-CDVTAQFLDETRAVMTKMOENLVRLGV 294
 Db 247 LVEFLGAGGEGEVMGNGYNGTKVAVSLKQSGMSPPAFLAENAIMLOLQHPRLVRYAV 306
 Oy 295 ILHGLTYMEVSKGNLVNFTGRALVNTAQLFSLHVAAGMELESKLVHNDIA 354
 Db 307 VTQPIITITTYEMKNGSLVDFLTKPSGKLVNKLMAOIAAGMAFIEQYNTIHRDLR 366
 Oy 355 ARNLIVSEDLVAVKVDGLAKA---ERKGLDSSRLPVKTPAPALKHGKTSKSDVWF 410
 Db 367 AANLIVSDTLSCRLADGLARLIEDNVTAREGAKPKIKMTAPALINVTFTIKSDVWF 426
 Oy 411 GVLIMEVSTGRAPYPMKSLKEVSEAVEKGYRMEPRCCPGPVHVLSSCWEADPARPP 470
 Db 427 GILTEIVTHTGRIPYPGMTNDEVYQNLGERYRVRPNDCPEELYLMLCWEKRPEDRPT 486
 Oy 471 FRKLAETL 478
 Db 487 FDYLRVYL 494

RESULT 12

OKHUK

protein-tyrosine kinase (EC 2.7.1.112) lck - human
 N:Alternate names: kinase-related transforming protein (lck)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #text, change 28-Jan-2000
 C:Accession: J00152; S07822; S07200; S01879; S07143; A32797; I57636
 C:Author: E. Van Huynh, T. de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
 Gene 84, 105-113, 1989

A:Title: Structure of the human lck gene: differences in genomic organisation within src
 A:Reference number: J00152; MUID:90108697; PMID:2558056
 A:Accession: J00152
 A:Molecule type: DNA
 A:Residues: 1-509 <ROU>
 A:Cross-references: EMBL:X14053
 R:Perlmutter, R.M.; March, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
 J. Cell. Biochem. 38, 117-126, 1988

A:Title: Structure and expression of lck transcripts in human lymphoid cells.
 A:Reference number: S07822; MUID:89123626; PMID:3265417
 A:Accession: S07822
 A:Molecule type: mRNA
 A:Residues: 1-86, 'P', '88-509' <PER>
 A:Cross-references: EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PID:g34295
 R:Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikata, Y.; Mak, T.W
 Eur. J. Immunol. 16, 1643-1646, 1986
 A:Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive h
 A:Reference number: S07200; MUID:87133831; PMID:3493155
 A:Accession: S07200
 A:Molecule type: mRNA
 A:Residues: 1-205, 'ASAIPPT', '212-257', 'RCGW', '262', 'TTT', '266', 'T', '268-281', 'AGRLP', '287-503',
 A:Cross-references: EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID:g36808
 R:Vellente, A.; Foss, F.M.; Sausville, E.A.; Bolten, J.B.; Rosen, N.
 Oncogene Res. 1, 357-374, 1987
 A:Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and othe
 A:Reference number: S01879; MUID:88217332; PMID:2835736
 A:Accession: S01879
 A:Molecule type: mRNA
 A:Residues: 368-471, 'H', '473-509' <VER>
 A:Cross-references: EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID:g34289
 R:Trevillian, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
 Biochim. Biophys. Acta 888, 286-295, 1986
 A:Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTR
 A:Reference number: S07143; MUID:87000726; PMID:3489486
 A:Accession: S07143
 A:Molecule type: mRNA
 A:Residues: 'A', '376-509' <TR>
 A:Cross-references: EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID:g35780
 R:Takadera, T.; Leung, S.; Gerone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak,
 Mol. Cell. Biol. 9, 2173-2180, 1989
 A:Title: Structure of the two promoters of the human lck gene: differential accumulat
 A:Reference number: A32797; MUID:89313764; PMID:2787474
 A:Accession: A32797

A:Molecule type: DNA
 A:Residues: 1-35 <TAK>
 A:Cross-references: GB:M26692; NID:g341523; PIDN:AAA59503.1; PID:g349702
 R:Garvin, A.M.; Pawar, S.; March, J.D.; Perlmutter, R.M.
 Mol. Cell. Biol. 8, 3058-3064, 1988
 A:Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma
 A:Reference number: 157636; MUID:89096891; PMID:2850479
 A:Accession: 157636
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-35, 'VR' <RR>
 A:Cross-references: GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:g553522
 C:Comment: Protein tyrosine kinases play important roles in the control of cell growth
 C:Genetics:
 A:Gene: GDB:119360; OMIM:153390
 A:Cross-references: GDB:119360; OMIM:153390
 A:Map position: 1p35-1p34.3
 A:Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
 C:Function:
 A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation;
 F:2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
 F:68-116/Domain: SH3 homology <SH3>
 F:127-224/Domain: SH2 homology <SH2>
 F:243-501/Domain: protein kinase homology <KIN>
 F:251-259/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3,5/Binding site: palmitate (Cys) (covalent) #status predicted
 F:273/Active site: lvs #status predicted
 F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status p

Query Match 27.8%; Score 742.5; DB 1; Length 509;
 Best Local Similarity 37.6%; Pred. No. 3.2e-31;
 Matches 161; Conservative 87; Mismatches 155; Indels 25; Gaps 9;
 Oy 65 GELAFRRGDVVTILEACENKSWYRKHTSGQEGILAAAGLREREALSADPKLSIMPFH 124
 Db 78 GDLFEKGEOLRIE--QSGEMKAOGLTGGEGFIDFNFAKANSLEPE-----PMWF 129

Db 78 GDLFEKGEQLRILE--QSGEMWKAQSLTTGEGFIPNFVAKANSLEPE-----PWFF 129
 QY 125 GKISGEAVOOLPPED--GLFLVRESARHPGDYLCV-----SFGDVIHYHVLHND-G 176
 Db 130 KNISRKDAERQLAPGNTGHSFLIRSESTAGSFSLSVRPFDQOGEVVAHYIRINDNG 189
 QY 177 HLTIIDEAVFECNLMDEVHYSKDKGAICTLVPRKRKHGKSAEELARAGMLLNLOHLT 236
 Db 190 GFYISPRITFPGLHELVIRHTNNSDGLCTRLSPQC---TQKPOKPMWDEMEVPRFTLK 246
 QY 237 LGAOIGERGAVLQGEHYLQ--KVAYKNIK-CDVTAQAFIDETAVMTKMOHENLVRLGY 294
 Db 247 LVERLAGOGEGEYVWMEYGNHTVAVKSLKQSGMSPDPAFLAEANLMOQLHQRVLRYAV 306
 QY 295 ILHOGYLVMEHYSKGNLVNLTGRALVNTAQLLOEFSLHVAEGMEYLESKLVHNDLA 354
 Db 307 VIOEPITITFEVWENGSVDFLKTTPSGIKTLTKLMDMAQIABGAFAIERKNYIHRDLK 366
 QY 355 ANILVSEDLVAVKVSDFGLAKA---ERKGLDSSRLPVKWTAPDALKHGFTSKSDVWSF 410
 Db 367 AANILVSDTLSCIKIADFGIARLTIEDNEYTAREGAKFPKWTAPDAEAINYGFTIKSDVWSF 426
 QY 411 GVLLMEFYSGRAPYPMKSLKEYSEANVEKGRMEPPGCGPVHVLSSGWEAPARPRP 470
 Db 427 GILTFELTVHGRIPYPMETNPEVLIQNLERGRVNRVPDNCPEELYLQMLRLCKWKERPEDPT 486
 QY 471 FRRLAEKL 478
 Db 487 FDLRLSVL 494

RESULT 13

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
 C/Species: Rous sarcoma virus
 C/Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Mar-2000
 C/Accession: S52313
 R./Tatosyan, A.; Yatsula, B.; Shlutman, M.; Molinova, E.; Kaverina, I.; Musatkina, E.; Les
 submitted to the EMBL Data Library, January 1995
 A/Description: Two new isoforms of v-src oncogene isolated from low and high metastatic
 A/Reference number: S52313
 A/Accession: S52313
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-545 <TAT>
 A/Cross-references: EMBL:X84074; NID:g663083; PIDN:CA58881.1; PID:g663084
 C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C/Keywords: ATP; autophosphorylation; blocked amino end; 1lipoprotein; myristylation; pnc
 F;108-157/Domain: SH3 homology <SH3>
 F;168-265/Domain: SH2 homology <SH2>
 F;285-543/Domain: protein kinase homology <KIN>
 F;293-301/Region: protein kinase ATP-binding motif
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F;315/Active site: Lys #status predicted
 F;436/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 27.6%; Score 736; DB 2; Length 545;
 Best Local Similarity 35.6%; Pred. No. 7.3e-31;
 Matches 187; Conservative 82; Mismatches 181; Indels 76; Gaps 16;
 QY 14 HGCDSAEELPR-----VSFRFLRAHNP-----PYSARMPRTTMAAGT----- 51
 Db 26 HGGFPASQPPKNTKAPLTAAPRSSR--RPPASQHRAAPDTHRRPSRF--GYANPEKLE 81
 QY 52 -----QCTKCEHTPPKPG-----ELAFRGADVTVTLEACENKSWYR 88
 Db 82 GDFNTSDYVTPSPGRATTLGAVTTFVALDYDESMITEDLSFKGERKQIYNNNEG-NNWL 140
 QY 89 VKHHTSGQSGLLAAGALREAREASADPKSLMFWERKISGQAVOOLPPED--GLFLV 146
 Db 141 AHSVTTGGQGYIPSNVAPSDSIQAE-----EMWYGKILTRRSSGRLLLPENPRGFLV 194
 QY 147 RESARRPBGVYLCVS-----FGRDVLIHYRLHND--GLHTIDEAVFECNLMDEVHYSKOK 200

Db 195 RESETTKGAVCLSVSDFDNAKGLNVKHYIKRLDSCGFIYTSRTQSSIQOLVAYYSKHA 254
 QY 201 GAICTLL--VPRRKIKGTSABEELARACMLNLNLOHLTGAQGEERPGAVLQGEHYLQ 257
 Db 255 DGLCHRLTNVCPSPKQOTOG---LAKDWEIPRESLRLEVKGQCCFEVWNGTWGTT 310
 QY 258 KVAYKNIK-CDVTAQAFIDETAVMTKMOHENLVRLGLVTLHOGYLVMEHYSKGNLVNLT 316
 Db 311 RVAIKTLRGTHSPPEAFLOEAOVYMKRLRHEKLVQLAVVSEETIYIVETMSGSLNLT 370
 QY 317 RFRGRALVNTAQLLOEFSLHVAEGMEYLESKLVHNDLAARNILVSEDLVAVKVSDFGLAKA 376
 Db 371 KGEVGRYTLRLPOLVDMAAQIASGMAYVERMNVYHRDLRAANILVGENLECKVADFGIARL 430
 QY 377 -----ERKGLDSSRLPVKWTAPDALKHGFTSKSDVWSFVLLMEFYSGRAPYPMKSLKE 432
 Db 431 IEDNEYTAROGAFAFPKWTAPDAEALGFRFTIISDVWSFGLTTELTKRVRPPGNGE 490
 QY 433 VSEAVEKGYRMEPPGCGPVHVLSSGWEAPARPRPRKLAELK 478
 Db 491 VLDREVRGYRMPCPPECPESLHDLMOQCMRREPEREPRTEYIQAOL 536

RESULT 14

TVCBS

protein-tyrosine kinase (EC 2.7.1.112) src - chicken
 N/Alternate names: kinase-related transforming protein src
 C/Species: Gallus gallus (chicken)
 C/Date: 19-Feb-1984 #sequence_revision 07-Oct-1994 #text_change 21-Jul-2000
 C/Accession: A00630; 150217; A41256; C35650; A32432
 R./Takeya, T.; Hanafusa, H.
 Cell 32, 881-890, 1983
 A/Title: Structure and sequence of the cellular gene homologous to the RSV src gene a
 A/Reference number: A00630; M01D:83155664; PMID:6293580
 A/Accession: A00630
 A/Molecule type: DNA
 A/Residues: 1-500, /R/, 502-533 <TAK>
 A/Cross-references: GB:J00844; NID:g212700
 R./Takeya, T.; Hanafusa, H.
 Cell 34, 319, 1983
 A/Reference number: A90838
 A/Contents: annotation; erratum, correct translation of residue 526
 R./Takeya, T.; Hanafusa, H.
 J. Virol. 44, 12-18, 1982
 A/Title: DNA sequence of the viral and cellular src gene of chickens: II comparison o
 A/Reference number: 150217; M01D:83059861; PMID:6292480
 A/Accession: 150217
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-7 <TAK>
 A/Cross-references: GB:J00908; NID:g211690; PIDN:AA48732.1; PID:g211691
 A/Note: the authors translated the codons AAC and CAG for residues 301 and 526 as Thr
 R./Doral, T.; Levy, J.B.; Kang, L.; Brugge, J.S.; Wang, L.H.
 Mol. Cell. Biol. 11, 4165-4176, 1991
 A/Title: Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5' exons and
 A/Reference number: A41256; M01D:91304409; PMID:1712905
 A/Accession: A41256
 A/Molecule type: mRNA
 A/Residues: 484-533 <DOR1>
 A/Cross-references: GB:S43579; NID:g1679964; PIDN:AA19353.1; PID:g233061
 A/Note: the authors translated the codon CAG for residue 527 as Glu
 R./Doral, T.; Wang, L.H.
 Mol. Cell. Biol. 10, 4068-4079, 1990
 A/Title: An alternative non-tyrosine protein kinase product of the c-src gene in chic
 A/Reference number: A35650; M01D:90318371; PMID:2115117
 A/Accession: C35650
 A/Molecule type: mRNA
 A/Residues: 1-182, /DPC1LPDSCIC' <DOR2>
 A/Cross-references: GB:M57290; NID:g212703; PIDN:AAA49078.1; PID:g212706
 A/Note: alternatively spliced mRNA exclusively replaces the long form in skeletal mus
 R./Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Maller, J.L.; Shalloway, D.

[illegible]

QY	410	FGVLLWEVFSYGRAPYPMKSLKEVSEAVEKGYRNEPPEGCGPYVHVLMSSCWEAEAPARR	469
Db	448	FGIILFELTTKGRVPYPMGNGEVLDRVERGYRMPCEPCPESLHDLMOQWRRDPERRP	507
QY	470	PERKLAEL	478
Db	508	TFEYLOAOL	516

Search completed: July 29, 2003, 09:53:03
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2003, 09:51:02 ; Search time 27 Seconds
(without alignments)
2230.045 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671
Sequence: 1 MAGRGLSVWRAHFGDSAE.....PASVSGDADGSPRSQEP 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2671	100.0	507	US-09-977-269-2	Sequence 2, Appl1
2	2671	100.0	507	US-09-977-260-2	Sequence 2, Appl1
3	2671	100.0	507	US-09-977-261-2	Sequence 2, Appl1
4	1245.5	46.6	450	US-09-977-269-7	Sequence 7, Appl1
5	1245.5	46.6	450	US-09-977-260-7	Sequence 7, Appl1
6	1245.5	46.6	450	US-09-977-261-7	Sequence 7, Appl1
7	1245.5	46.6	450	US-10-059-585-42	Sequence 42, Appl1
8	1245.5	46.6	450	US-10-177-293-88	Sequence 88, Appl1
9	1245.5	46.6	450	US-10-298-377A-2	Sequence 2, Appl1
10	916	34.3	357	US-09-929-266-9	Sequence 9, Appl1
11	768	28.8	258	US-09-840-704-3	Sequence 3, Appl1
12	742.5	27.8	509	US-09-977-269-18	Sequence 18, Appl1
13	742.5	27.8	509	US-09-977-260-18	Sequence 18, Appl1
14	742.5	27.8	509	US-09-977-261-18	Sequence 18, Appl1
15	727	27.2	536	US-09-977-269-13	Sequence 13, Appl1

16	727	27.2	536	10	US-09-977-260-13	Sequence 13, Appl1
17	727	27.2	536	11	US-09-929-266-10	Sequence 10, Appl1
18	727	27.2	536	11	US-09-977-261-13	Sequence 13, Appl1
19	720.5	27.0	505	9	US-09-977-269-17	Sequence 17, Appl1
20	720.5	27.0	505	10	US-09-977-260-17	Sequence 17, Appl1
21	720.5	27.0	505	11	US-09-977-261-17	Sequence 17, Appl1
22	710	26.6	543	9	US-09-977-269-14	Sequence 14, Appl1
23	710	26.6	543	10	US-09-977-260-14	Sequence 14, Appl1
24	710	26.6	543	11	US-09-977-261-14	Sequence 14, Appl1
25	710	26.6	543	16	US-10-298-377A-4	Sequence 16, Appl1
26	707	26.5	512	9	US-09-977-269-16	Sequence 16, Appl1
27	707	26.5	512	10	US-09-977-260-16	Sequence 16, Appl1
28	707	26.5	512	11	US-09-977-261-16	Sequence 16, Appl1
29	699.5	26.2	536	9	US-09-977-269-12	Sequence 12, Appl1
30	699.5	26.2	536	10	US-09-977-260-12	Sequence 12, Appl1
31	699.5	26.2	536	11	US-09-977-261-12	Sequence 12, Appl1
32	699	26.2	499	9	US-09-977-269-19	Sequence 19, Appl1
33	699	26.2	499	10	US-09-977-260-19	Sequence 19, Appl1
34	699	26.2	499	11	US-09-977-261-19	Sequence 19, Appl1
35	698.5	26.2	537	9	US-09-977-269-11	Sequence 11, Appl1
36	698.5	26.2	537	10	US-09-977-260-11	Sequence 11, Appl1
37	698.5	26.2	537	11	US-09-977-261-11	Sequence 11, Appl1
38	695.5	26.0	537	10	US-09-771-161A-212	Sequence 212, App
39	695.5	26.0	537	10	US-09-771-161A-213	Sequence 213, App
40	692	25.9	505	10	US-09-771-161A-186	Sequence 186, App
41	681.5	25.5	529	9	US-09-977-269-15	Sequence 15, Appl1
42	681.5	25.5	529	10	US-09-977-260-15	Sequence 15, Appl1
43	681.5	25.5	529	11	US-09-977-261-15	Sequence 15, Appl1
44	660.5	24.7	822	14	US-10-003-295-4	Sequence 4, Appl1
45	654.5	24.5	505	9	US-09-977-269-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1	
US-09-977-269-2	
Sequence 2, Application US/09977269	
Patent No. US20020082037A1	
GENERAL INFORMATION:	
APPLICANT: ULIRICH, AXEL	
APPLICANT: GISHIZKY, MIKHAIL	
APPLICANT: SUDES, IRINGCARD	
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES	
FILE REFERENCE: 038602/1260	
CURRENT APPLICATION NUMBER: US/09/977, 269	
CURRENT FILING DATE: 2001-10-16	
PRIOR APPLICATION NUMBER: 08/232,545	
PRIOR FILING DATE: 1994-04-22	
NUMBER OF SEQ ID NOS: 24	
SOFTWARE: PatentIn Ver. 2.1	
SEQ ID NO 2	
LENGTH: 507	
TYPE: PRT	
ORGANISM: Unknown Organism	
FEATURE:	
OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte	
OTHER INFORMATION: Kinase 1	
US-09-977-269-2	
Query Match	100.0%; Score 2671; DB 9; Length 507;
Best Local Similarity	100.0%; Pred. No. 6.7e+209;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MAGRGLSVWRAHFGDSAEELPRVSRFLRAMHPPVSAMPTRRNAPGTCITKCEHT 60
DB	1 MAGRGLSVWRAHFGDSAEELPRVSRFLRAMHPPVSAMPTRRNAPGTCITKCEHT 60
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DB	61 RPKGELAFRRKGDVVTLEACENKSWYRVKHTSGDGLLAAGALRREALSADPKSLM 120
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Db      121 PMFHGKISGOEAVOOLPPEDGLFVRESARHPGDVLCVSGRDVTHYRVLHRDGLTI 180
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Qy      241 IGEGERGAVLQGEYLGOKVAVKNIKCDVTAQAFLDETAVMTKMOHENLVRLGLVILHOGI 300
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Qy      301 YIYMEHVSCKGNLVNFLTGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360
Db      301 YIYMEHVSCKGNLVNFLTGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360
Qy      361 SEDLVAKVSDPGLAKAEKRGKLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 420
Db      361 SEDLVAKVSDPGLAKAEKRGKLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 420
Qy      421 GRAPYPMKSLKEVSEAVEKGYRMEPEGCSPVHVLMSSCWEAEAPARRPFRKLAEKLAR 480
Db      421 GRAPYPMKSLKEVSEAVEKGYRMEPEGCSPVHVLMSSCWEAEAPARRPFRKLAEKLAR 480
Qy      481 ELRSAGAPASVSGODADGSTSPRSQEP 507
Db      481 ELRSAGAPASVSGODADGSTSPRSQEP 507

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RESULT 2

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US-09-977-260-2
; Sequence 2, Application US/09977260
; Publication No. US20020192790A1
; GENERAL INFORMATION:
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1260
; CURRENT APPLICATION NUMBER: US/09/977, 260
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232, 545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
; OTHER INFORMATION: kinase 1
US-09-977-260-2

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Query Match      100.0%; Score 2671; DB 10; Length 507;
Best Local Similarity 100.0%; Pred. No. 6, 7e-209;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAGRGSLSVWRAFHGCDSAEEIPLRVSPRFLRAWHPPVSAARMPTRRMAPGTQCTITKCEHT 60
Db      1 MAGRGSLSVWRAFHGCDSAEEIPLRVSPRFLRAWHPPVSAARMPTRRMAPGTQCTITKCEHT 60
Qy      61 RRPFGELARPKGDVYITILEACENKSWYRYKHNHTSGOEGLLAAGALRERALSADPKLSLM 120
Db      61 RRPFGELARPKGDVYITILEACENKSWYRYKHNHTSGOEGLLAAGALRERALSADPKLSLM 120
Qy      121 PMFHGKISGOEAVOOLPPEDGLFVRESARHPGDVLCVSGRDVTHYRVLHRDGLTI 180
Db      121 PMFHGKISGOEAVOOLPPEDGLFVRESARHPGDVLCVSGRDVTHYRVLHRDGLTI 180
Qy      181 DEAVFECNLMADWEHYSKDKGALCTKLVPRKRKHGTSABEELARAGWMLNLOHLTLGAQ 240
Db      181 DEAVFECNLMADWEHYSKDKGALCTKLVPRKRKHGTSABEELARAGWMLNLOHLTLGAQ 240

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Qy      241 IGEGERGAVLQGEYLGOKVAVKNIKCDVTAQAFLDETAVMTKMOHENLVRLGLVILHOGI 300
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Qy      301 YIYMEHVSCKGNLVNFLTGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360
Db      301 YIYMEHVSCKGNLVNFLTGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360
Qy      361 SEDLVAKVSDPGLAKAEKRGKLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 420
Db      361 SEDLVAKVSDPGLAKAEKRGKLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 420
Qy      421 GRAPYPMKSLKEVSEAVEKGYRMEPEGCSPVHVLMSSCWEAEAPARRPFRKLAEKLAR 480
Db      421 GRAPYPMKSLKEVSEAVEKGYRMEPEGCSPVHVLMSSCWEAEAPARRPFRKLAEKLAR 480
Qy      481 ELRSAGAPASVSGODADGSTSPRSQEP 507
Db      481 ELRSAGAPASVSGODADGSTSPRSQEP 507

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RESULT 3

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US-09-977-261-2
; Sequence 2, Application US/09977261
; Publication No. US20030054527A1
; GENERAL INFORMATION:
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977, 261
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232, 545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
; OTHER INFORMATION: kinase 1
US-09-977-261-2

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Query Match      100.0%; Score 2671; DB 11; Length 507;
Best Local Similarity 100.0%; Pred. No. 6, 7e-209;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MAGRGSLSVWRAFHGCDSAEEIPLRVSPRFLRAWHPPVSAARMPTRRMAPGTQCTITKCEHT 60
Qy      61 RRPFGELARPKGDVYITILEACENKSWYRYKHNHTSGOEGLLAAGALRERALSADPKLSLM 120
Db      61 RRPFGELARPKGDVYITILEACENKSWYRYKHNHTSGOEGLLAAGALRERALSADPKLSLM 120
Qy      121 PMFHGKISGOEAVOOLPPEDGLFVRESARHPGDVLCVSGRDVTHYRVLHRDGLTI 180
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Qy      181 DEAVFECNLMADWEHYSKDKGALCTKLVPRKRKHGTSABEELARAGWMLNLOHLTLGAQ 240
Db      181 DEAVFECNLMADWEHYSKDKGALCTKLVPRKRKHGTSABEELARAGWMLNLOHLTLGAQ 240
Qy      241 IGEGERGAVLQGEYLGOKVAVKNIKCDVTAQAFLDETAVMTKMOHENLVRLGLVILHOGI 300
Db      241 IGEGERGAVLQGEYLGOKVAVKNIKCDVTAQAFLDETAVMTKMOHENLVRLGLVILHOGI 300
Qy      301 YIYMEHVSCKGNLVNFLTGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360
Db      301 YIYMEHVSCKGNLVNFLTGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360

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Dd      8  WPGSTECIAKYAHNFGHAEDDLPEFCGDVLTITVAATKDPNNYKAKANKV-GRGGITIPANYQ 66

QY      107  EREALSADPKLSLMPWFHKGISGDEAVOOLPDEDDGLFVLRESARHPDGYLVCSFGD 166
Dd      67  KREGVACAGTKLSLMPWFHKGITRDEAERLLYPETGTLFVLRSTNYPGDYTLCSDCGKY 126

QY      167  IHRVLYHROCHLTIDAVFPCNLMMWVEHYSKDKCAITKTVPRPKRHGTSABEELARA 226
Dd      127  EHRIRMYHASKLSIDEEVFEMLQVLEHTYSDDAGLCTRLIKRKNMGEYVAAODEYRS 166

QY      227  GWLLNLQHLTLGAQIGEGEFGAVLOGEYLGQKVAVANKIKCDVTAAQLDETAVYTKQNE 286
Dd      187  GMAIANKKEIKLTLQTIKGCEGDYMLGCDYRGKNVAAKCIKNDAQAQLAEASVYTOLRHS 246

QY      287  NLVRLILGVLIIHQ--GLIYIMEHVSNGNLVNFRTFGRALVTATQOLFOSLIHVAGMEYLE 344
Dd      247  NLVQLLGVLVEEGGGLITVETMAWGSVDYLRSGKSVLOGDCLLFSLDVCBAMEYLE 306

QY      345  SKRLVHRDLAARNIILVSEDLVAKVSDPGLAKERKGLDSSRLPYKMTAPALAKHGFTSK 404
Dd      307  GNFVHRDLAARNVLVSESDNVAKVSDPGLTKRASTQDTGRLPKMTAPALAKRKRSTK 366

QY      405  SDVWSGCVLLMEYFSTGRAPYRKMSLKEYSVAVEKGYMEPBECCPGCVHYVLLSSCEAE 464
Dd      367  SDVWSGCVLLMEYSPGRVYPRIPRLKDVPRVEKGYKMDAPDCPAVEYVWKNCWMLD 426

QY      465  PARPPEPKLAERL 478
Dd      427  AAMRPSFLDLREQL 440

RESULT 6
US-09-977-261-7
: Sequence 7, Application US/09977261
: Publication No. US20030054527A1
: GENERAL INFORMATION:
: APPLICANT: ULLRICH, AXEL
: APPLICANT: GISHIZKY, MIKHAIL
: APPLICANT: SORES, IRMINGARD
: TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
: FILE REFERENCE: 038602/1259
: CURRENT APPLICATION NUMBER: US/09/977,261
: CURRENT FILING DATE: 2001-10-16
: PRIORITY APPLICATION NUMBER: 08/7332,545
: PRIORITY FILING DATE: 1994-04-22

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APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortodagyl, Gabriel N.
APPLICANT: Pusztai, Lajos

RESULT 9
US-10-298-377A-2
Sequence 2, Application US//10298377A
Publication No. US20030130209A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Chersesh, David A.
APPLICANT: Paul, Robert

RESULT 10
US-09-929-266-9
Sequence 9, Application US/09929266
Publication No. US20030045694A1
GENERAL INFORMATION:
APPLICANT: Brian T. Chalt
APPLICANT: Darin R. Latimer
APPLICANT: Paul M. Lizardi
APPLICANT: Eric R. Kershner
APPLICANT: Jon S. Morrow
APPLICANT: Matthew E. Roth
APPLICANT: Martin J. Matlessich

Query Match	28.88;	Score 768;	DB 10;	Length 258;
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36 / AANILVSDTLESCIADEFGIARLIEDNEYAREGAKFPKIMYAPEAINYGTITIKSDVMSF 426

Publication No. US20030054527A1

; LENGTH: 536

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-269-13

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Query Match	27.2%;	Score 727;	DB 9;	Length 536;
Best Local Similarity	35.2%;	Pred. No. 7.8e-51;		
Matches 182;	Conservative 83;	Mismatches 178;	Indels 74;	Gaps 14;

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      101 TDISFKGGERLDIVNNTG--DWMLNHSLSSTQGTQIPENYAPADSDIOAE-----EWF 1533
QY      125 GKISGGEAYQOOLOPED--GLFYRESARHGDDVLYCS-----FGRDVIYRYVLND-G 1766
      154 GKITRESERLLMNMENPRGTFLVASEETTGATCALSDDPDNKGKLVNHYKTKRIKIDSG 2133
QY      177 HLTIDEAVFPCIMDMVNEHYSKDKALCTKL--VRPKRHGTSAEBELARAGWLNLOH 2341
      214 GFYTSRTQFNFSLOOLIVAYYSKHNAGDLCHRLTTCPTSKPOTOG---LAKDAWEIIPRES 2659
QY      235 LITGAOIGGEGFAYLOGEYLG--OKVAYKNIK--CDVTAQOALDETAVMTKQHNINVRLL 2922
      270 LRIEVLKLOGGCGEGEYMGWGTNGTTFVALKTKLPGTMSFEALDQEOYKKRIKHEKLYOLT 3299
QY      293 GVTLHOGVLYVNEHYSKGNLVNFLTGRALVNTAOLLQFSLHVAEGMEYLESKLVIHRD 3523
      330 AVYSEPIITYEVMYSKSGSLDIFDLTGEGTKTLRLPLQVDMAAQIASGMAYVERNYVHRD 3869
QY      353 LAARNILVSEDIIVAYKSDFGGLAKA-----ERKGDSRLPYKWTAPALAKGKTEKSDW 4088
      390 LRANILVGENILYCKVADFGELKRLLEDNEYIAROGACAKPLIKWTAPREALYIGRFTISDW 4499
QY      409 SFGVLLMEVYSGRAPYRMSLKEYSEAVERYGRNEDEPQCGRVNHYLMSGCEWAEFARR 4688
      450 SFGILLTELTTGGRVYDPEGMVREVLVDQYERKGRYRMPCCPCEBSIHLIMOCQMKPEER 5099
QY      469 PPRKRLAEKLARELSAGAPASVOSQDDGDSISPRSQ 505
      510 PTFEYLOAFU-----EDFTSTERYO 531

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Search completed: July 29, 2003, 09:53:36
Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2003, 09:49:12 ; Search time 20 Seconds
(without alignments)
1072.580 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671

Sequence: 1 MAGRGLVSMRAPHGCSAE.....PASVSGDADGSPRSQEP 507

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents-AA:*
2: /cgn2.6/ptodata/1/1aa/5A.COMB.pep:*
3: /cgn2.6/ptodata/1/1aa/5B.COMB.pep:*
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5: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2671	100.0	507	US-08-426-509A-2	Sequence 2, Appl1
2	2671	100.0	507	US-08-232-545-2	Sequence 2, Appl1
3	2671	100.0	507	PCR-US95-05008-2	Sequence 2, Appl1
4	2664	99.7	507	US-08-604-989A-5	Sequence 5, Appl1
5	2445	91.5	527	US-09-315-928-2	Sequence 2, Appl1
6	2444	91.5	466	US-08-604-989A-4	Sequence 2, Appl1
7	2434	91.1	528	US-08-876-882-2	Sequence 2, Appl1
8	2012	75.3	386	US-09-741-154-4	Sequence 4, Appl1
9	2012	75.3	415	US-09-741-154-2	Sequence 2, Appl1
10	1269	47.5	246	US-08-604-989A-3	Sequence 3, Appl1
11	1245.5	46.6	450	US-08-426-509A-7	Sequence 7, Appl1
12	1245.5	46.6	450	US-08-232-545-7	Sequence 7, Appl1
13	1245.5	46.6	450	PCR-US95-05008-7	Sequence 7, Appl1
14	797	29.8	269	US-08-701-191A-35	Sequence 35, Appl1
15	768	28.8	258	US-09-035-706-3	Sequence 3, Appl1
16	768	28.8	258	US-08-955-841-3	Sequence 3, Appl1
17	768	28.8	258	US-09-390-425-3	Sequence 3, Appl1
18	768	28.8	258	US-09-566-906-3	Sequence 3, Appl1
19	742.5	27.8	509	US-09-039-555B-17	Sequence 17, Appl1
20	742.5	27.8	509	US-08-426-509A-18	Sequence 18, Appl1
21	742.5	27.8	509	US-09-457-040B-8	Sequence 8, Appl1
22	742.5	27.8	509	US-08-232-545-18	Sequence 18, Appl1
23	742.5	27.8	509	PCR-US95-05008-18	Sequence 18, Appl1
24	732	27.4	533	US-07-820-011A-2	Sequence 2, Appl1
25	732	27.4	533	PCR-US93-00445-2	Sequence 2, Appl1
26	727	27.2	536	US-07-820-011A-4	Sequence 4, Appl1
27	727	27.2	536	US-08-426-509A-13	Sequence 13, Appl1

28	727	27.2	536	US-08-232-545-13	Sequence 13, Appl1
29	727	27.2	536	PCR-US93-00445-4	Sequence 4, Appl1
30	727	27.2	536	PCR-US95-05008-13	Sequence 13, Appl1
31	720.5	27.0	505	US-08-426-509A-17	Sequence 17, Appl1
32	720.5	27.0	505	US-08-232-545-17	Sequence 17, Appl1
33	720.5	27.0	505	PCR-US95-05008-17	Sequence 17, Appl1
34	710	26.6	543	US-08-426-509A-14	Sequence 14, Appl1
35	710	26.6	543	US-08-232-545-14	Sequence 14, Appl1
36	710	26.6	543	PCR-US95-05008-14	Sequence 14, Appl1
37	707	26.5	512	US-08-426-509A-16	Sequence 16, Appl1
38	707	26.5	512	US-08-232-545-16	Sequence 16, Appl1
39	707	26.5	512	PCR-US95-05008-16	Sequence 16, Appl1
40	699.5	26.2	536	US-08-426-509A-12	Sequence 12, Appl1
41	699.5	26.2	536	US-08-232-545-12	Sequence 12, Appl1
42	699.5	26.2	536	PCR-US95-05008-12	Sequence 12, Appl1
43	699	26.2	499	US-08-426-509A-19	Sequence 19, Appl1
44	699	26.2	499	US-08-232-545-19	Sequence 19, Appl1
45	699	26.2	499	PCR-US95-05008-19	Sequence 19, Appl1

ALIGNMENTS

RESULT 1
US-08-426-509A-2
; Sequence 2, Application US/08426509A
; Patent No. 6326469
; GENERAL INFORMATION:
; APPLICANT: Viliitch, Axel
; APPLICANT: Gishlitzky, Mikhail
; APPLICANT: Sures, Irman G.
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
; TITLE OF INVENTION: TYROSINE KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York,
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,509A
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/232,545
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 507 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: NO. 6326469e
; US-08-426-509A-2
Query Match 100.0%, Score 2671; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 2.7e-219;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 DEAVFPCNLMDMVEHYSKDGAICTKLVPRKRKHGTSABEELARAGMLNLQHLTLGAQ 240
DB 181 DEAVFPCNLMDMVEHYSKDGAICTKLVPRKRKHGTSABEELARAGMLNLQHLTLGAQ 240
QY 241 IGESEFGAVLQGEYLQGVAVKNIKCDVTAQAFLEDTAVMTKQHENLVRLGLVILHOG 300
DB 241 IGESEFGAVLQGEYLQGVAVKNIKCDVTAQAFLEDTAVMTKQHENLVRLGLVILHOG 300
QY 301 YIWEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
DB 301 YIWEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
QY 361 SEDLVAKVSDFGGLAKAERKGLDSSRLPVKWTAPALKHGKFTSKSDVMSFGVLLMEVFSY 420
DB 361 SEDLVAKVSDFGGLAKAERKGLDSSRLPVKWTAPALKHGKFTSKSDVMSFGVLLMEVFSY 420
QY 421 GRAPYPMASLKEYSEAVEKGYRMEPPGCGPVHYVLMSCWEAPARPPFRKLAELAR 480
DB 421 GRAPYPMASLKEYSEAVEKGYRMEPPGCGPVHYVLMSCWEAPARPPFRKLAELAR 480
QY 481 ELSAGAPASVSGODADGSTSPRSQEP 507
DB 481 ELSAGAPASVSGODADGSTSPRSQEP 507

RESULT 2
US-08-232-545-2
: Sequence 2, Application US/08232545
: Patent No. 6506578
: GENERAL INFORMATION:
: APPLICANT: Ullrich, Axel
: APPLICANT: Gishizsky, Mikhail
: APPLICANT: Sures, Irman G.
: TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine
: TITLE OF INVENTION: Kinases
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennile & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232,545
: FILING DATE: 22-APR-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Cortuzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7683-050
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)790-9090
: TELEFAX: (212)869-9741
: TELEX: 66141 PENNIE

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: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 507 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: US-08-232-545-2

Query Match 100.0%; Score 2671; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 2.7e-219;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGGSLVSWRAFHGCDASAEELPRVSPRFLRAHMPPVVSARMPTRRPAAGTQITKCEHT 60
DB 1 MAGGSLVSWRAFHGCDASAEELPRVSPRFLRAHMPPVVSARMPTRRPAAGTQITKCEHT 60
QY 61 RPRKGELAFRRKGDVVTLLACENKSWYRVKHHSTSGOGLLAAGALRREALSADPKLSLM 120
DB 61 RPRKGELAFRRKGDVVTLLACENKSWYRVKHHSTSGOGLLAAGALRREALSADPKLSLM 120
QY 121 PWFHKGKISGQEAQQOQPPEDGFLVRESARHNGDYVLCVSGRDVYHYRVLHRDGLTI 180
DB 121 PWFHKGKISGQEAQQOQPPEDGFLVRESARHNGDYVLCVSGRDVYHYRVLHRDGLTI 180
QY 181 DEAVFPCNLMDMVEHYSKDGAICTKLVPRKRKHGTSABEELARAGMLNLQHLTLGAQ 240
DB 181 DEAVFPCNLMDMVEHYSKDGAICTKLVPRKRKHGTSABEELARAGMLNLQHLTLGAQ 240
QY 241 IGESEFGAVLQGEYLQGVAVKNIKCDVTAQAFLEDTAVMTKQHENLVRLGLVILHOG 300
DB 241 IGESEFGAVLQGEYLQGVAVKNIKCDVTAQAFLEDTAVMTKQHENLVRLGLVILHOG 300
QY 301 YIWEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
DB 301 YIWEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
QY 361 SEDLVAKVSDFGGLAKAERKGLDSSRLPVKWTAPALKHGKFTSKSDVMSFGVLLMEVFSY 420
DB 361 SEDLVAKVSDFGGLAKAERKGLDSSRLPVKWTAPALKHGKFTSKSDVMSFGVLLMEVFSY 420
QY 421 GRAPYPMASLKEYSEAVEKGYRMEPPGCGPVHYVLMSCWEAPARPPFRKLAELAR 480
DB 421 GRAPYPMASLKEYSEAVEKGYRMEPPGCGPVHYVLMSCWEAPARPPFRKLAELAR 480
QY 481 ELSAGAPASVSGODADGSTSPRSQEP 507
DB 481 ELSAGAPASVSGODADGSTSPRSQEP 507

RESULT 3
PCT-US95-05008-2
: Sequence 2, Application PC/TUS9505008
: GENERAL INFORMATION:
: APPLICANT: Sugen, Inc.
: APPLICANT: 515 Galveston Drive
: APPLICANT: Redwood City, California 94063-4720
: APPLICANT: United States of America
: APPLICANT: Wissenschaften E.V.
: APPLICANT: Munchen 80539
: APPLICANT: Germany
: TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
: TITLE OF INVENTION: Kinases
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennile & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-2

Query Match 100.0%; Score 2671; DB 5; Length 507;
Best Local Similarity 100.0%; Pred. No. 2,7e-219;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGRGSLSVSRARHGCDSAEELPRVSPRFLRAMHPPVVSARMPTRRAPSTGCTTKEHT 60
DB 1 MAGRGSLSVSRARHGCDSAEELPRVSPRFLRAMHPPVVSARMPTRRAPSTGCTTKEHT 60
QY 61 RPKRGELAFRRKGDVVTILEACENKSWYRVKHNHTSGOGLAAGALRREALSADPKISLM 120
DB 61 RPKRGELAFRRKGDVVTILEACENKSWYRVKHNHTSGOGLAAGALRREALSADPKISLM 120
QY 121 PWFHKGISGQEAVALQPPEDGLFLVRESARHPGDVYLVSFGSDVTHYRVLRHGDHLTI 180
DB 121 PWFHKGISGQEAVALQPPEDGLFLVRESARHPGDVYLVSFGSDVTHYRVLRHGDHLTI 180
QY 181 DEAVFPCNLMDMVEHYSKDKGALCTKLVPRKRKHGTSABEELARAGWMLNLOHLTGAO 240
DB 181 DEAVFPCNLMDMVEHYSKDKGALCTKLVPRKRKHGTSABEELARAGWMLNLOHLTGAO 240
QY 241 IGESEGAVALQGEYLQKVAVKNIKCDVTAQAFLEDTAVMTKMOHENLVRLGLVILHOG 300
DB 241 IGESEGAVALQGEYLQKVAVKNIKCDVTAQAFLEDTAVMTKMOHENLVRLGLVILHOG 300
QY 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
DB 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
QY 361 SEDLVAKVSDPGLAKARERKGLDSSRLPVKWTAPALKHGFTSKSDVMSGVLLMEVFSY 420
DB 361 SEDLVAKVSDPGLAKARERKGLDSSRLPVKWTAPALKHGFTSKSDVMSGVLLMEVFSY 420
QY 421 GRAPYPMLSLKEVSEAVEKGYRMEPPGCGPGYHVLMSCWEAEPARPPFRKLAEKLAR 480
DB 421 GRAPYPMLSLKEVSEAVEKGYRMEPPGCGPGYHVLMSCWEAEPARPPFRKLAEKLAR 480
QY 481 ELRSAGAPASVSGODADGSTSPRSQEP 507
DB 481 ELRSAGAPASVSGODADGSTSPRSQEP 507

RESULT 4
US-08-604-989A-5
; Sequence 5, Application US/08604989A

Patent No. 5834208
GENERAL INFORMATION:
APPLICANT: Sakano, S.
TITLE OF INVENTION: NO. 5834208el Tyrosine kinase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,989A
FILING DATE: February 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles E. Miller
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 1920-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human
STRAIN: UT-7
US-08-604-989A-5

Query Match 99.7%; Score 2664; DB 2; Length 507;
Best Local Similarity 99.8%; Pred. No. 1e-218;
Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAGRGSLSVSRARHGCDSAEELPRVSPRFLRAMHPPVVSARMPTRRAPSTGCTTKEHT 60
DB 1 MAGRGSLSVSRARHGCDSAEELPRVSPRFLRAMHPPVVSARMPTRRAPSTGCTTKEHT 60
QY 61 RPKRGELAFRRKGDVVTILEACENKSWYRVKHNHTSGOGLAAGALRREALSADPKISLM 120
DB 61 RPKRGELAFRRKGDVVTILEACENKSWYRVKHNHTSGOGLAAGALRREALSADPKISLM 120
QY 121 PWFHKGISGQEAVALQPPEDGLFLVRESARHPGDVYLVSFGSDVTHYRVLRHGDHLTI 180
DB 121 PWFHKGISGQEAVALQPPEDGLFLVRESARHPGDVYLVSFGSDVTHYRVLRHGDHLTI 180
QY 181 DEAVFPCNLMDMVEHYSKDKGALCTKLVPRKRKHGTSABEELARAGWMLNLOHLTGAO 240
DB 181 DEAVFPCNLMDMVEHYSKDKGALCTKLVPRKRKHGTSABEELARAGWMLNLOHLTGAO 240
QY 241 IGESEGAVALQGEYLQKVAVKNIKCDVTAQAFLEDTAVMTKMOHENLVRLGLVILHOG 300
DB 241 IGESEGAVALQGEYLQKVAVKNIKCDVTAQAFLEDTAVMTKMOHENLVRLGLVILHOG 300
QY 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
DB 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
QY 361 SEDLVAKVSDPGLAKARERKGLDSSRLPVKWTAPALKHGFTSKSDVMSGVLLMEVFSY 420
DB 361 SEDLVAKVSDPGLAKARERKGLDSSRLPVKWTAPALKHGFTSKSDVMSGVLLMEVFSY 420
QY 421 GRAPYPMLSLKEVSEAVEKGYRMEPPGCGPGYHVLMSCWEAEPARPPFRKLAEKLAR 480
DB 421 GRAPYPMLSLKEVSEAVEKGYRMEPPGCGPGYHVLMSCWEAEPARPPFRKLAEKLAR 480

Db 421 GRAPYKMSLKESEAVEKGYRMEPEGCGPVHVLMSCEWEAPRRPFRKLAEKLAR 480
QY 481 ELRSAGAPASVSGODADGSTSPRSQ 507
Db 481 ELRSAGAPASVSGODADGSTSPRSQ 507

RESULT 5
US-09-315-928-2

; Sequence 2, Application US/09315928
; Patent No. 6368796
; GENERAL INFORMATION:
; APPLICANT: Groopman, Jerome E.
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; FILE REFERENCE: NEH97-01PZ
; CURRENT APPLICATION NUMBER: US/09/315,928
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 08/876,882
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 60/035,228
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-315-928-2

Query Match 91.5%; Score 2445; DB 4; Length 527;
Best Local Similarity 93.5%; Pred. No. 4.9e-200;
Matches 472; Conservative 1; Mismatches 18; Indels 14; Gaps 2;

QY 1 MAGRGLSVWRAFHGCDSEELPRVSPRLRAMHPPVSARMPTRRMAGTQCITKCEHT 60
Db 1 MAGRGLSVWRAFHGCDSEELPRVSPRLRAMHPPVSARMPTRRMAGTQCITKCEHT 60
QY 61 RRPGLRLARKGDVVTLLACENKSMYRKHNHSGOGLLAAGALREBRLSADPKLSLM 120
Db 61 RRPGLRLARKGDVVTLLACENKSMYRKHNHSGOGLLAAGALREBRLSADPKLSLM 120
QY 121 PMFHGKISGOEAVOOLQPPEDGLFLVRESARHPGDVLCVSGRDVYIHRVLRDGLTI 180
Db 121 PMFHGKISGOEAVOOLQPPEDGLFLVRESARHPGDVLCVSGRDVYIHRVLRDGLTI 180
QY 181 DEAVFPCNLMDVNEHYSKDKGAICTKLVRPKRHGKTSABEELARAGWLLNLOHLTLGAO 240
Db 181 DEAVFPCNLMDVNEHYSKDKGAICTKLVRPKRHGKTSABEELARAGWLLNLOHLTLGAO 240
QY 241 IGEGERGAVLQGEYLGOKVAVNKICDVTAAFLDETAAMTKMOHNLVRLIGVTLHOGT 300
Db 241 IGEGERGAVLQGEYLGOKVAVNKICDVTAAFLDETAAMTKMOHNLVRLIGVTLHOGT 300
QY 301 YVMEHVSNGNLVNLRTGRALVNTAQLQFSLHYAEGMEYLESKKLVHRDLAARNILY 360
Db 301 YVMEHVSNGNLVNLRTGRALVNTAQLQFSLHYAEGMEYLESKKLVHRDLAARNILY 360
QY 361 SEDLVAKVSDPGLAARERKGLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 420
Db 361 SEDLVAKVSDPGLAARERKGLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 420
QY 421 GRAPYKMSLKESEAVEKGYRMEPEGCGPVHVLMSCEWEAPRRPFRKLAEKLAR 480
Db 421 GRAPYKMSLKESEAVEKGYRMEPEGCGPVHVLMSCEWEAPRRPFRKLAEKLAR 480
QY 481 ELRSAGAPASVSGODADGSTSPRSQ 505
Db 481 ELRSAGAPASVSGODADGSTSPRSQ 505
QY 470 ---SANNPRSMGPGSTAYVOPPPSQ 491
Db 470 ---SANNPRSMGPGSTAYVOPPPSQ 491

RESULT 6
US-08-604-989A-4

; Sequence 4, Application US/08604989A
; Patent No. 5834208
; GENERAL INFORMATION:
; APPLICANT: Sakano, S.
; TITLE OF INVENTION: No. 5834208el Tyrosine Kinase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,989A
; FILING DATE: February 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles E. Miller
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 1920-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: human
; STRAIN: UT-7
US-08-604-989A-4

Query Match 91.5%; Score 2444; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 5e-200;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 MPTRRMAGTQCITKCEHTRPKPGELARFKGDVVTLLACENKSMYRKHNHSGOGLLA 101
Db 1 MPTRRMAGTQCITKCEHTRPKPGELARFKGDVVTLLACENKSMYRKHNHSGOGLLA 101
QY 102 AGALREBRLSADPKLSLMPMFHGISSGOEAVOOLQPPEDGLFLVRESARHPGDVLCVS 161
Db 102 AGALREBRLSADPKLSLMPMFHGISSGOEAVOOLQPPEDGLFLVRESARHPGDVLCVS 161
QY 162 FGRDVIHVRVLRDGLTIIDEAVFPCNLMDVNEHYSKDKGAICTKLVRPKRHGKTSABE 221
Db 162 FGRDVIHVRVLRDGLTIIDEAVFPCNLMDVNEHYSKDKGAICTKLVRPKRHGKTSABE 221
QY 222 ELARAGWLLNLOHLTLGAOIGEGERGAVLQGEYLGOKVAVNKICDVTAAFLDETAAMT 281
Db 222 ELARAGWLLNLOHLTLGAOIGEGERGAVLQGEYLGOKVAVNKICDVTAAFLDETAAMT 281
QY 282 KMÖHENLVRLIGVTLHOGTYVMEHVSNGNLVNLRTGRALVNTAQLQFSLHYAEGME 341
Db 282 KMÖHENLVRLIGVTLHOGTYVMEHVSNGNLVNLRTGRALVNTAQLQFSLHYAEGME 341
QY 342 YLESKLVHRDLAARNILVSEDLVAKVSDPGLAARERKGLDSSRLPVKWTAPALKHGFT 401
Db 342 YLESKLVHRDLAARNILVSEDLVAKVSDPGLAARERKGLDSSRLPVKWTAPALKHGFT 401
QY 402 TSKSDVMSFGVLLMEVFSYGRAPYKMSLKESEAVEKGYRMEPEGCGPVHVLMSCEW 461
Db 402 TSKSDVMSFGVLLMEVFSYGRAPYKMSLKESEAVEKGYRMEPEGCGPVHVLMSCEW 461

Db 361 TSXSDVMSFGVLLMEVFSYGRAPYPKMSLKEVSEAVEKGRMEPECGPGVHVLMSSCW 420
Qy 462 EAEPRARPPRKLAEKLAELRSAGAPASVSGODADGSTSPRSOEP 507
Db 421 EAEPRARPPRKLAEKLAELRSAGAPASVSGODADGSTSPRSOEP 466

RESULT 7

US-08-876-882-2
Sequence 2, Application US/08876882
Patent No. 5981201
GENERAL INFORMATION:
APPLICANT: Avraham, Hava
APPLICANT: Groopman, Jerome E.
TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT
TITLE OF INVENTION: OF BREAST CANCER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876,882
FILING DATE: 16-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,228
FILING DATE: 08-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Doreen, Hogle M
REGISTRATION NUMBER: 36,361
REFERENCE/DOCKET NUMBER: NEDH97-01PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-876-882-2

Query Match 91.1%; Score 2434.5; DB 2; Length 528;
Best Local Similarity 93.3%; Pred. No. 3.8e-199;
Matches 472; Conservative 1; Mismatches 18; Indels 15; Gaps 3;

Qy 1 MAGGSLVSMRAPHGCSAEELPRVSRFLRAMHPVVSARMPRRRPAFTGCTTCKEHT 60
Db 1 MAGGSLVSMRAPHGCSAEELPRVSRFLRAMHPVVSARMPRRRPAFTGCTTCKEHT 60
Qy 61 RPKRGELAFRRKGDVVTI-LEACEKSMYRYKHNHTSGOGLLAAGALREKLSADPKLTSL 119
Db 61 RPKRGELAFRRKGDVVTI-LEACEKSMYRYKHNHTSGOGLLAAGALREKLSADPKLTSL 120
Qy 120 MPWFHGRISGOEAVQOLQPPEDGLFLVRESARHPGDVLCVSGRDVIHYRVLRDGHILT 179
Db 121 MPWFHGRISGOEAVQOLQPPEDGLFLVRESARHPGDVLCVSGRDVIHYRVLRDGHILT 180
Qy 180 IDEAVFFCNLMQVVEHYSKDKGALCTKLVPRKRGKHSAAEELARAGWMLNLOHITLGA 239
Db 181 IDEAVFFCNLMQVVEHYSKDKGALCTKLVPRKRGKHSAAEELARAGWMLNLOHITLGA 240

Qy 240 QIGEGFAGVLOGEYLQOKAVVNIKCDVTAQAEFLDETAVMTKMQHENYVRLGLVILHOG 299
Db 241 QIGEGFAGVLOGEYLQOKAVVNIKCDVTAQAEFLDETAVMTKMQHENYVRLGLVILHOG 300
Qy 300 LYIVMEHVSNGNLVNLRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNIL 359
Db 301 LYIVMEHVSNGNLVNLRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNIL 360
Qy 360 VSEDVAKVSDPGLAKERRGGLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFS 419
Db 361 VSEDVAKVSDPGLAKERRGGLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFS 419
Qy 420 YGRAPYPKMSLKEVSEAVEKGRMEPECGPGVHVLMSSCWEAEPRARPPRKLAEKLA 479
Db 420 YGRAPYPKMSLKEVSEAVEKGRMEPECGPGVHVLMSSCWEAEPRARPPRKLAEKLA 470
Qy 480 RELRSAGAPASVSGODADGSTSPRSQ 505
Db 471 ----SAMPWRSPGSAVAVQVPPSPQ 492

RESULT 8

US-09-741-154-4
Sequence 4, Application US/09741154
Patent No. 6437110
GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen M. et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CLO01061
CURRENT APPLICATION NUMBER: US/09/741,154
CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 386
TYPE: PRT
ORGANISM: Human
US-09-741-154-4

Query Match 75.3%; Score 1012; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.4e-163;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 WFHGRISGOEAVQOLQPPEDGLFLVRESARHPGDVLCVSGRDVIHYRVLRDGHILT 181
Db 1 WFHGRISGOEAVQOLQPPEDGLFLVRESARHPGDVLCVSGRDVIHYRVLRDGHILT 180
Qy 182 EAEPRARPPRKLAEKLAELRSAGAPASVSGODADGSTSPRSOEP 507
Db 182 EAEPRARPPRKLAEKLAELRSAGAPASVSGODADGSTSPRSOEP 507
Qy 61 EAEPRARPPRKLAEKLAELRSAGAPASVSGODADGSTSPRSOEP 507
Db 61 EAEPRARPPRKLAEKLAELRSAGAPASVSGODADGSTSPRSOEP 507
Qy 242 GEGFAGVLOGEYLQOKAVVNIKCDVTAQAEFLDETAVMTKMQHENYVRLGLVILHOG 301
Db 121 GEGFAGVLOGEYLQOKAVVNIKCDVTAQAEFLDETAVMTKMQHENYVRLGLVILHOG 300
Qy 302 LYIVMEHVSNGNLVNLRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNIL 359
Db 181 LYIVMEHVSNGNLVNLRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNIL 360
Qy 362 EDVAKVSDPGLAKERRGGLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFS 419
Db 241 EDVAKVSDPGLAKERRGGLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFS 418
Qy 422 YGRAPYPKMSLKEVSEAVEKGRMEPECGPGVHVLMSSCWEAEPRARPPRKLAEKLA 479
Db 301 YGRAPYPKMSLKEVSEAVEKGRMEPECGPGVHVLMSSCWEAEPRARPPRKLAEKLA 470
Qy 482 RELRSAGAPASVSGODADGSTSPRSQ 505
Db 361 RELRSAGAPASVSGODADGSTSPRSQ 492

RESULT 9
US-09-741-154-2
; Sequence 2, Application US/09741154
; Patent No. 6437110
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen M. et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01061
; CURRENT APPLICATION NUMBER: US/09/741,154
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRN
; ORGANISM: Human
US-09-741-154-2

Query Match 75.3%; Score 2012; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.6e-163;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 MFHGKISGGEAVQQLPPEDGLFLVRESARHPGDYLCVSGFDVHYHYRLHARDGHLTD 181
DB 30 MFHGKISGGEAVQQLPPEDGLFLVRESARHPGDYLCVSGFDVHYHYRLHARDGHLTD 89
QY 182 EAFVPCNLMVMHYHYSKDKAICTKLYPRKRHGTSAEELARAGMLNLQHLTGAQI 241
DB 90 EAFVPCNLMVMHYHYSKDKAICTKLYPRKRHGTSAEELARAGMLNLQHLTGAQI 149
QY 242 GEGEFAGVLGEGYLGOKVAVKNIKCDVTAQAFIDETAVMTKMOHENLVRLGLVILHOGLY 301
DB 150 GEGEFAGVLGEGYLGOKVAVKNIKCDVTAQAFIDETAVMTKMOHENLVRLGLVILHOGLY 209
QY 302 IYMEHVSCKNLVNFRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHBDLAARNILVS 361
DB 210 IYMEHVSCKNLVNFRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHBDLAARNILVS 269
QY 362 EDVYAVSPDGLAKARKKGLDSSRLPYKWTAPALHKGRTSKSDVWSEVLLMEVFSYG 421
DB 270 EDVYAVSPDGLAKARKKGLDSSRLPYKWTAPALHKGRTSKSDVWSEVLLMEVFSYG 329
QY 422 RAYPKMSLKEVSEAVEKGYRMPPEGCPGVHVLMSCEAEAPARRPPRKLAEKLARE 481
DB 330 RAYPKMSLKEVSEAVEKGYRMPPEGCPGVHVLMSCEAEAPARRPPRKLAEKLARE 389
QY 482 LRSAGAPASVSGODADGSTSPRSQEP 507
DB 390 LRSAGAPASVSGODADGSTSPRSQEP 415

RESULT 10
US-08-604-989A-3
; Sequence 3, Application US/08604989A
; Patent No. 5834208
; GENERAL INFORMATION:
; APPLICANT: Sakano, S.
; TITLE OF INVENTION: No. 5834208el Tyrosine kinase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,989A
FILING DATE: February 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles E. Miller
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 1920-026
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human
STRAIN: UT-7
US-08-604-989A-3

Query Match 47.5%; Score 1269; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 2.4e-100;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 QHLLTGAQIGEGFAGVLGEGYLGOKVAVKNIKCDVTAQAFIDETAVMTKMOHENLVRL 292
DB 1 QHLLTGAQIGEGFAGVLGEGYLGOKVAVKNIKCDVTAQAFIDETAVMTKMOHENLVRL 60
QY 293 GVLILHOGLYIYMEHVSCKNLVNFRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHBD 352
DB 61 GVLILHOGLYIYMEHVSCKNLVNFRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHBD 120
QY 353 LAARNILVSEBDVAVKVSDFGLAKARKKGLDSSRLPYKWTAPALHKGRTSKSDVWSEV 412
DB 121 LAARNILVSEBDVAVKVSDFGLAKARKKGLDSSRLPYKWTAPALHKGRTSKSDVWSEV 180
QY 413 LMEVFSYGRAPPKMSLKEVSEAVEKGYRMPPEGCPGVHVLMSCEAEAPARRPPR 472
DB 181 LMEVFSYGRAPPKMSLKEVSEAVEKGYRMPPEGCPGVHVLMSCEAEAPARRPPR 240
QY 473 KLAEKL 478
DB 241 KLAEKL 246

RESULT 11
US-08-426-509A-7
; Sequence 7, Application US/08426509A
; Patent No. 6326469
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Gishizky, Mikhail
; APPLICANT: Sures, Irman G.
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
; TITLE OF INVENTION: TYROSINE KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,509A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,545
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-0074-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: NO. 6326459e
US-08-426-509A-7

Db	307	GNNEFVRDLAARAVLVSSENNVAKVSDFGLTKEASSTODTGLPKMTAPALAEKFEFTK	366
QY	405	SDWSPGCVLLMEFSEGRAPYPKMSLKEYSAEKGYMRPEECPCQPVHVLMSGCEAE	464
Db	367	SDWSPGCVLLMEFSEGRAPYPRITPLKDYPRVEKGIKMDAPDCQPAVTEVKNCHLD	426
QY	465	PARRPPFRKLAEKL	478
Db	427	AAMRPSFLQREQL	440
RESULT 14			
US-08-701-191A-35			
: Sequence 35, Application US/08701191A			
: Patent No. 5942428			
GENERAL INFORMATION:			
APPLICANT: Moosa Mohammadi, Joseph Schlessinger,			
APPLICANT: and Stevan R. Hubbard			
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN			
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE			
NUMBER OF SEQUENCES: 41			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Lyon & Lyon			
STREET: 633 West Fifth Street			
STREET: Suite 4700			
CITY: Los Angeles			
STATE: California			
COUNTRY: U.S.A.			
ZIP: 90071-2066			
COMPUTER READABLE FORM:			
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb			
MEDIUM TYPE: storage			
COMPUTER: IBM Compatible			
OPERATING SYSTEM: IBM P.C. DOS 5.0			
SOFTWARE: PASTSEO for Windows 2.0			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/701,191A			
FILING DATE: August 21, 1996			
CLASSIFICATION: 530			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER:			
FILING DATE:			
ATTORNEY/AGENT INFORMATION:			
NAME: Warburg, Richard J.			
REGISTRATION NUMBER: 32,327			
REFERENCE/DOCKET NUMBER: 227/088			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (213) 489-1600			
TELEFAX: (213) 955-0440			
TELEX: 67-3510			
INFORMATION FOR SEQ. ID NO: 35:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 269 amino acids			
TYPE: amino acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: protein			
US-08-701-191A-35			
Query Match			
Best Local Similarity 58.7%; Score 797; DB 2; Length 269;			
Matches 152; Conservative 46; Mismatches 59; Indels 2; Caps 1			
QY	222	ELARAWLNLQHLITGAQIGCEGCAVLOGEYLGQKVAAYANIKCDVTAQAFIDETRAVMT	281
Db	1	EFRRSGWALNMEKELKLTQITGKEGEGDVALDDYRGKNVAVKCIINDATAQAFIAEASVMT	60
QY	282	KMOHEMIVRLATGIVLHQ-GLYIVMEHVSCKNLVNFLTRGRALVNTAQLQPSLVAEG	339
Db	61	QLRHSNLVQLGIVYEKSGGLITVEYMAKSDIVDYLRRSRVSIVGGDCILKFSIDVCEA	120
QY	340	MEYLSKSLVHDLAARNILVSEDIYAKVSPFGIAKAEKRGKDDSSRLPVKMTAPAEALKHG	399

DB 121 MEYLEGNFVHRLAARNVLSVDNVAKVSDFGLTKKASSTPDGKLPVKWTAPALREK 180
QY 400 KFTSKSDVWSFGVLLMEYFSYGRAPYPMKSLKEVSEAVEKGYRMEPPGCGPVPVHLMSS 459
DB 181 KFTSKSDVWSFGVLLMEYFSYGRAPYPMKSLKEVSEAVEKGYRMEPPGCGPVPVHLMSS 240
QY 460 CMEAEPPARRPFRKLAERL 478
DB 241 CWHLDAMRPSFLQRL 259

RESULT 15

US-09-035-706-3
; Sequence 3, Application US/09035706
; Patent No. 6001622
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Integrin-Linked Kinase and
; TITLE OF INVENTION: Its Uses
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: KIN-2CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 258 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-035-706-3

Query Match 28.8%; Score 768; DB 3; Length 258;
Best Local Similarity 58.8%; Pred. No. 1.2e-57;
Matches 147; Conservative 45; Mismatches 56; Indels 2; Gaps 1;

QY 231 NLQHLITLGAQIGEGEFGVLOGEYLIGQVAAVKNIKCDYTAQAFLEDTAVYTKMQHENLYR 290
DB 1 NMKEIKLQTTGGKEFGVMDYRGNKVAVKIKNDATAQAFLEASVMTQLRHSNLYQ 60
QY 291 LLGYLIHO--GLYIYMEHVSNGNLYNFLTGRGALVNTAQLLOPSLHYAEGMEYLESKKL 348
DB 61 LLGYIYERKGLIYITEYMAKGSIVDYLRSGRSVYLGDCILKFSLDVCEAMEYLEGNNF 120
QY 349 VHRDLAARNILVSEDLVAKVSDPGLAKAERKGLDSSRLPVKWTAPALRHGKFTSKSDVW 408
DB 121 VHRDLAARNVLSVDNVAKVSDFGLTKKASSTPDGKLPVKWTAPALREKKFTSKSDVW 180

QY 409 SEGVLLMEYFSYGRAPYPMKSLKEVSEAVEKGYRMEPPGCGPVPVHLMSSCMEAEPPARR 468
DB 181 SFGIILMEYFSYGRAPYPMKSLKEVSEAVEKGYRMEPPGCGPVPVHLMSSCMEAEPPARR 240
QY 469 PFRKLAERL 478
DB 241 PSFLQRL 259

Search completed: July 29, 2003, 09:52:34
Job time : 22 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2003, 09:46:12 ; Search time 44 Seconds

(without alignments)
1828.963 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671

Sequence: 1 MAGRSLVSMRAFHCDSAE.....PASVSGDDADGSTRSPRQEP 507

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: *
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25: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2671	100.0	507	AA1980	Cytoplasmic tyrosin
2	2671	100.0	507	AA1981	Human mark-related
3	2668	99.9	507	AA1982	Megakaryocyte kina
4	2444	91.5	466	AA1983	N-terminal truncat
5	2434.5	91.1	528	AA1984	Human mark protein
6	2012	75.3	415	AA1985	Human kinase relat
7	1261	47.2	246	AA1986	Tyrosine kinase do
8	1247.5	46.7	459	AA1987	Human polyptide
9	1245.5	46.6	450	AA1988	Wild-type human c-

10	1245.5	46.6	450	AA1989	PKA substrate, Csk
11	1245.5	46.6	450	AA1990	Amino acid sequenc
12	1245.5	46.6	450	AA1991	Amino acid sequenc
13	1245.5	46.6	450	AA1992	Amino acid sequenc
14	1245.5	46.6	450	AA1993	Breast cancer asso
15	979.5	36.7	820	AA1994	Drosophila melanog
16	916	34.3	357	AA1995	Human SH2/SH3 doma
17	753	28.2	502	AA1996	Fugu rubripes lymph
18	745	27.9	567	AA1997	Tumour involved ge
19	742.5	27.8	508	AA1998	Human lymphocyte k
20	736.5	27.6	509	AA1999	PKA substrate, Src
21	735	27.5	533	AA2000	Chicken pp60 c-src
22	733	27.4	533	AA2001	Wild-type chicken
23	733	27.4	533	AA2002	Mutant chicken c-S
24	733	27.4	533	AA2003	Amino acid sequenc
25	727	27.2	533	AA2004	Mutant chicken c-S
26	727	27.2	536	AA2005	Human pp60 c-src p
27	727	27.2	536	AA2006	Human v-src isoform
28	727	27.2	536	AA2007	Human SH2/SH3 doma
29	727	27.2	536	AA2008	Human src-c protei
30	724	27.1	1504	AA2009	Drosophila melanog
31	720.5	27.0	505	AA2010	Human tyrosine kin
32	718	26.9	542	AA2011	Novel human protei
33	714	26.7	541	AA2012	Mouse src-c protei
34	710	26.6	543	AA2013	Novel human diagno
35	710	26.6	543	AA2014	Amino acid sequenc
36	708	26.5	541	AA2015	Perinuclear theca
37	708	26.5	543	AA2016	Human yes1 protei
38	701.5	26.3	1130	AA2017	Human Bcr-Abl tyro
39	699.5	26.2	565	AA2018	Novel human diagno
40	699.5	26.2	1130	AA2019	Human Bcr-Abl tyro
41	699.5	26.2	1130	AA2020	Human Bcr-Abl tyro
42	698.5	26.2	1130	AA2021	Human Bcr-Abl tyro
43	698.5	26.2	1130	AA2022	Human Bcr-Abl tyro
44	698.5	26.2	1130	AA2023	Human Bcr-Abl tyro
45	697.5	26.1	1130	AA2024	Human Bcr-Abl tyro

ALIGNMENTS

RESULT 1	ID	AA1980 standard; protein: 507 AA.	Location/Qualifiers
AA1980	AA1980	25-MAR-2003 (updated)	cytoplasmic tyrosine kinase.
AA1981	AA1981	27-OCT-1995 (first entry)	cytoplasmic tyrosine kinase; blood; cell differentiation;
AA1982	AA1982		screening; anticancer agent; SH3; src homology domain.
AA1983	AA1983		Human SH2/SH3 doma
AA1984	AA1984		Fugu rubripes lymph
AA1985	AA1985		Tumour involved ge
AA1986	AA1986		Human lymphocyte k
AA1987	AA1987		PKA substrate, Src
AA1988	AA1988		Chicken pp60 c-src
AA1989	AA1989		Wild-type chicken
AA1990	AA1990		Mutant chicken c-S
AA1991	AA1991		Amino acid sequenc
AA1992	AA1992		Mutant chicken c-S
AA1993	AA1993		Human pp60 c-src p
AA1994	AA1994		Human v-src isoform
AA1995	AA1995		Human SH2/SH3 doma
AA1996	AA1996		Human src-c protei
AA1997	AA1997		Drosophila melanog
AA1998	AA1998		Human tyrosine kin
AA1999	AA1999		Novel human protei
AA2000	AA2000		Mouse src-c protei
AA2001	AA2001		Novel human diagno
AA2002	AA2002		Amino acid sequenc
AA2003	AA2003		Perinuclear theca
AA2004	AA2004		Human yes1 protei
AA2005	AA2005		Human Bcr-Abl tyro
AA2006	AA2006		Novel human diagno
AA2007	AA2007		Human Bcr-Abl tyro
AA2008	AA2008		Human Bcr-Abl tyro
AA2009	AA2009		Human Bcr-Abl tyro
AA2010	AA2010		Human Bcr-Abl tyro
AA2011	AA2011		Human Bcr-Abl tyro
AA2012	AA2012		Human Bcr-Abl tyro
AA2013	AA2013		Human Bcr-Abl tyro
AA2014	AA2014		Human Bcr-Abl tyro
AA2015	AA2015		Human Bcr-Abl tyro
AA2016	AA2016		Human Bcr-Abl tyro
AA2017	AA2017		Human Bcr-Abl tyro
AA2018	AA2018		Human Bcr-Abl tyro
AA2019	AA2019		Human Bcr-Abl tyro
AA2020	AA2020		Human Bcr-Abl tyro
AA2021	AA2021		Human Bcr-Abl tyro
AA2022	AA2022		Human Bcr-Abl tyro
AA2023	AA2023		Human Bcr-Abl tyro
AA2024	AA2024		Human Bcr-Abl tyro

XX (ASAH) ASAH KASEI KOGYO KK.
 XX Sakano S;
 PI WPI; 1995-106842/14.
 DR N-PSDB; AA084888.
 XX
 PT Cytoplasmic tyrosine kinase and antibody recognising it - for
 PT screening chemical substances for tyrosine kinase inhibitory or
 PT activating activity for use as cancer therapy
 XX
 PS Claim 1; Page 42-44; 58pp; English.
 XX
 CC A cytoplasmic tyrosine kinase which has enhanced expression in
 CC connection with blood cell differentiation has been isolated from the
 CC human U9-7 blood cell line. The DNA sequences and antibodies raised
 CC against the enzyme, are useful for screening agents for inhibiting or
 CC activating activity on the tyrosine kinase, for use as anticancer agents.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 507 AA;
 Query Match 100.0%; Score 2671; DB 16; Length 507;
 Best Local Similarity 100.0%; Pred. No. 8.6e-242;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAGRGLVSWRAHFGDSAEELPRVSPRLRAHNPVPSARMPTRRMAGTCTTCENT 60
 1 MAGRGLVSWRAHFGDSAEELPRVSPRLRAHNPVPSARMPTRRMAGTCTTCENT 60
 61 RPKPGLARFKGDVVTILEACENKSWYRVKHNHSGOGLLAAGALREREALSDPKLSLM 120
 61 RPKPGLARFKGDVVTILEACENKSWYRVKHNHSGOGLLAAGALREREALSDPKLSLM 120
 121 PMFHGKISGOEAVOQLOPPEDGLFLVRESARHPGDVYLVSFGRDVIHYRVLHRDGLTI 180
 121 PMFHGKISGOEAVOQLOPPEDGLFLVRESARHPGDVYLVSFGRDVIHYRVLHRDGLTI 180
 181 DEAVFPCNLMADWEHNSKDKGALCTKLVPRKRKHGKTSABEELARAGWMLNQLTLGAQ 240
 181 DEAVFPCNLMADWEHNSKDKGALCTKLVPRKRKHGKTSABEELARAGWMLNQLTLGAQ 240
 241 IGEFEGAVLQGEYLGOKYAVKNIKCDVTAQAFIDETAAMTKQHENVLLGLVILHOG 300
 241 IGEFEGAVLQGEYLGOKYAVKNIKCDVTAQAFIDETAAMTKQHENVLLGLVILHOG 300
 301 YIYMEHVSKNLVNPLRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILY 360
 301 YIYMEHVSKNLVNPLRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILY 360
 361 SEDLVAKVSDPGLAKERKGLDSSRLPVKWTAPALAKHGFYKSDVMSFGVILMEVFSY 420
 361 SEDLVAKVSDPGLAKERKGLDSSRLPVKWTAPALAKHGFYKSDVMSFGVILMEVFSY 420
 421 GRAPYPKMSLKEVSEAVEKGYRMEPEGCGPVHYVLMSSCWEAEPARPPFRKLAEKLAR 480
 421 GRAPYPKMSLKEVSEAVEKGYRMEPEGCGPVHYVLMSSCWEAEPARPPFRKLAEKLAR 480
 481 ELRSAGAPASVSGODADGSTSPRSQEP 507
 481 ELRSAGAPASVSGODADGSTSPRSQEP 507

RESULT 2
 ID AA015860 standard; Protein; 507 AA.
 AC AA015860;
 DT 02-JAN-2003 (first entry)
 XX Human matk-related protein.

XX Human; allergic disease; matk gene; atopic dermatitis.
 KM Homo sapiens.
 OS WO200275304-A1.
 PN 26-SEP-2002.
 PD 01-MAR-2002; 2002WO-JP01916.
 PF 21-MAR-2001; 2001JP-0081028.
 PR (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN AGENCY NATION.
 PI Sugita Y, Heishi M, Kagaya S, Gunji S, Tsujimoto G;
 PT WPI; 2002-750572/81.
 DR N-PSDB; AAL50631.
 XX
 PT Examining allergic diseases by changes in expression level of matk gene
 PT in peripheral monocytes as indication, also applicable in screening
 PT compounds for treating allergic diseases e.g. atopic dermatitis -
 XX Disclosure; Page 52-55; 60pp; Japanese.
 XX
 CC The invention comprises a method of examining allergic diseases, the
 CC method comprises comparing the expression level of the matk gene in a
 CC biological sample of a patient and a healthy individual. The method of
 CC the invention is useful for examining/diagnosing allergic diseases -
 CC particularly atopic dermatitis, the method of the invention is also
 CC useful in screening candidate compounds for remedies. The present amino
 CC acid sequence represents a human matk-related protein.
 XX
 SQ Sequence 507 AA;
 Query Match 100.0%; Score 2671; DB 23; Length 507;
 Best Local Similarity 100.0%; Pred. No. 8.6e-242;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAGRGLVSWRAHFGDSAEELPRVSPRLRAHNPVPSARMPTRRMAGTCTTCENT 60
 1 MAGRGLVSWRAHFGDSAEELPRVSPRLRAHNPVPSARMPTRRMAGTCTTCENT 60
 61 RPKPGLARFKGDVVTILEACENKSWYRVKHNHSGOGLLAAGALREREALSDPKLSLM 120
 61 RPKPGLARFKGDVVTILEACENKSWYRVKHNHSGOGLLAAGALREREALSDPKLSLM 120
 121 PMFHGKISGOEAVOQLOPPEDGLFLVRESARHPGDVYLVSFGRDVIHYRVLHRDGLTI 180
 121 PMFHGKISGOEAVOQLOPPEDGLFLVRESARHPGDVYLVSFGRDVIHYRVLHRDGLTI 180
 181 DEAVFPCNLMADWEHNSKDKGALCTKLVPRKRKHGKTSABEELARAGWMLNQLTLGAQ 240
 181 DEAVFPCNLMADWEHNSKDKGALCTKLVPRKRKHGKTSABEELARAGWMLNQLTLGAQ 240
 241 IGEFEGAVLQGEYLGOKYAVKNIKCDVTAQAFIDETAAMTKQHENVLLGLVILHOG 300
 241 IGEFEGAVLQGEYLGOKYAVKNIKCDVTAQAFIDETAAMTKQHENVLLGLVILHOG 300
 301 YIYMEHVSKNLVNPLRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILY 360
 301 YIYMEHVSKNLVNPLRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILY 360
 361 SEDLVAKVSDPGLAKERKGLDSSRLPVKWTAPALAKHGFYKSDVMSFGVILMEVFSY 420
 361 SEDLVAKVSDPGLAKERKGLDSSRLPVKWTAPALAKHGFYKSDVMSFGVILMEVFSY 420
 421 GRAPYPKMSLKEVSEAVEKGYRMEPEGCGPVHYVLMSSCWEAEPARPPFRKLAEKLAR 480
 421 GRAPYPKMSLKEVSEAVEKGYRMEPEGCGPVHYVLMSSCWEAEPARPPFRKLAEKLAR 480

OY 481 ELRSAGAPASVSGODADGTSRSPSOEP 507
 |||||||
 DB 481 ELRSAGAPASVSGODADGTSRSPSOEP 507

RESULT 3
 AAR84181
 ID AAR84181 standard; Protein; 507 AA.
 XX AAR84181;

AC AAR84181;
 DT 26-MAR-1996 (first entry)

DE Megakaryocyte kinase MKK1.

KM Megakaryocyte kinase-1; MKK1; cytoplasmic tyrosine kinase;
 KW cellular signal transduction; leukaemia; thrombocytopenia.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 48..111
 FT /label= SH3_domain

FT Domain 122..196
 FT /label= SH2_domain

FT Domain 233..478
 FT /label= Catalytic_domain

PN W09529185-A1.

XX 02-NOV-1995.

PD 24-APR-1995; 95WO-US05008.

PR 21-APR-1995; 95US-0426509.

PR 22-APR-1994; 94US-0232545.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA (SUOE-) SUGEN INC.

PI Gishizky M, Sures I, Ullrich A;

DR WPI; 1995-382959/49.

DR N-PSDB; AAT00616.

PT New poly:nucleotide(s) encoding megakaryocyte tyrosine kinase(s) -
 PT used to develop prods. for the treatment and diagnosis of kinase
 PT related signal transduction abnormalities.

PS Claim 15; Fig 1A-C; 82pp; English.

CC Human megakaryocyte kinase MKK1 (AAR84181) is a 58 kDa cytosolic
 CC tyrosine kinase showing 54% homology with csk. It appears to play
 CC a regulatory role in the growth and differentiation of

CC megakaryocytes and perhaps neural tissues. Recombinant MKK1 can be
 CC produced in host cells by expression of encoding cDNA (AAT00616), and
 CC used in the treatment and diagnosis of e.g. leukaemia and
 CC thrombocytopenia.

XX SQ Sequence 507 AA;

Query Match 99.9%; Score 2668; DB 16; Length 507;

Best Local Similarity 99.8%; Pred. No. 1.6e-241;

Matches 506; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGRSLVSWRAFHGCDSEBELPRVSPRFLRAWHPPVSARMPTRRMAPGTQCTKCEHT 60
 |||||||

DB 1 MAGRSLVSWRAFHGCDSEBELPRVSPRFLRAWHPPVSARMPTRRMAPGTQCTKCEHT 60
 |||||||

OY 61 RPKBELAFRRKGDVYTIIEACENKSWRYKHHHTSQOEBLLAAGALREDAISADPKLSLM 120
 |||||||

DB 61 RPKBELAFRRKGDVYTIIEACENKSWRYKHHHTSQOEBLLAAGALREDAISADPKLSLM 120
 |||||||

OY 121 PWFHCKISQGEAVOOLQPPEDGLFLYRESARHPGDVILCVSPGRDYIHYRVLHRDGHLLTI 180
 |||||||
 DB 121 PWFHCKISQGEAVOOLQPPEDGLFLYRESARHPGDVILCVSPGRDYIHYRVLHRDGHLLTI 180
 |||||||
 OY 181 DEAVFEFCNMDVMEHYHNSKDKGAICTKLVPRKRHGTKSAEELARAGWLLNLOHLLTGAO 240
 |||||||
 DB 181 DEAVFEFCNMDVMEHYHNSKDKGAICTKLVPRKRHGTKSAEELARAGWLLNLOHLLTGAO 240
 |||||||
 OY 241 IGEGERGAVLQGEYTGOKVAVNKNICDVTQAQFLDETVAMTQMOHBNLVRLGLVILHGL 300
 |||||||
 DB 241 IGEGERGAVLQGEYTGOKVAVNKNICDVTQAQFLDETVAMTQMOHBNLVRLGLVILHGL 300
 |||||||
 OY 301 YIVMEHVSQGNLVNFLTFRGRALVMTAOLQPSLVHAEQMEYLESKKLVHRLAARNILV 360
 |||||||
 DB 301 YIVMEHVSQGNLVNFLTFRGRALVMTAOLQPSLVHAEQMEYLESKKLVHRLAARNILV 360
 |||||||
 OY 361 SEDLVAKVSDFGTAKAERKGLDSSRLPVKMTAPEALKHGFPSKSDVMSFGVLLMEVFSY 420
 |||||||
 DB 361 SEDLVAKVSDFGTAKAERKGLDSSRLPVKMTAPEALKHGFPSKSDVMSFGVLLMEVFSY 420
 |||||||
 OY 421 GRAPYPRKMSLKEVSEAVEKGYMPEPEGCGPVHYLMSSCWEAEAPARRPPFKKLAEKLAR 480
 |||||||
 DB 421 GRAPYPRKMSLKEVSEAVEKGYMPEPEGCGPVHYLMSSCWEAEAPARRPPFKKLAEKLAR 480
 |||||||
 OY 481 ELRSAGAPASVSGODADGTSRSPSOEP 507
 |||||||
 DB 481 ELRSAGAPASVSGODADGTSRSPSOEP 507
 |||||||

RESULT 4
 AAR71132
 ID AAR71132 standard; Protein; 466 AA.

XX AAR71132;

AC 25-MAR-2003 (updated)

DT 27-OCT-1995 (first entry)

DE N-terminal truncated cytoplasmic tyrosine kinase.

XX cytoplasmic; tyrosine kinase; blood; cell differentiation;
 KW screening; anticancer agent; SH3; src homology domain.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 7..70
 FT /note= "SH3 domain"

FT Domain 81..155
 FT /note= "SH2 domain"

FT Domain 192..438
 FT /note= "tyrosine kinase domain"

PN W09506113-A1.

PD 02-MAR-1995.

PF 25-AUG-1994; 94WO-JP01411.

PR 25-AUG-1993; 93JP-0210403.

PR 29-MAR-1994; 94JP-0058553.

XX (ASAH) ASAH1 KASEI KOGYO KK.

PI Sakano S;

DR WPI; 1995-106842/14.

DR N-PSDB; AAO8488.

XX Cytoplasmic tyrosine kinase and antibody recognising it - for
 PT screening chemical substances for tyrosine kinase inhibitory or
 PT activating activity for use as cancer therapy

PS Claim 1; Page 40-42; 58pp; English.

XX A cytoplasmic tyrosine kinase which has enhanced expression in
 CC connection with blood cell differentiation has been isolated from the
 CC human ut-7 blood cell line. This sequence comprises an N-terminal
 CC truncated fragment of the enzyme (residues 42-507 of AAR71133). The DNA
 CC sequences and antibodies raised against the enzyme, are useful for
 CC screening agents for inhibiting or activating activity on the tyrosine
 CC kinase, for use as anticancer agents.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SO Sequence 466 AA:

Query Match 91.5%; Score 2444; DB 16; Length 466;
 Best Local Similarity 100.0%; Pred. No. 1.6e-220;
 Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 MPTRRRNPQCTCKCKEHTPRKPGELAFKRGDVTITLACENKSWYKVNHTSGOGLLA 101
 DB 1 MPTRRRNPQCTCKCKEHTPRKPGELAFKRGDVTITLACENKSWYKVNHTSGOGLLA 60
 QY 102 AGALRRREALSDPKLSLMPFHKISGOEAVOOLPPEDGLFLVRESARHPGDYVLCVS 161
 DB 61 AGALRRREALSDPKLSLMPFHKISGOEAVOOLPPEDGLFLVRESARHPGDYVLCVS 120
 QY 162 FGRDVIHYRYLHRDGLHTIDEAVFPCNLMDVHEHYSKDKGALCTKLVRPRKHKGTSAEE 221
 DB 121 FGRDVIHYRYLHRDGLHTIDEAVFPCNLMDVHEHYSKDKGALCTKLVRPRKHKGTSAEE 180
 QY 222 ELARAGMLNLQHLTTGAQIGEGEFGAVLOGEYLGQVAVKNIKCDVTAQAFIDEAVMT 281
 DB 181 ELARAGMLNLQHLTTGAQIGEGEFGAVLOGEYLGQVAVKNIKCDVTAQAFIDEAVMT 240
 QY 282 KMCHENLVRLGLYLHOGILTYMEHYSKGNLVNLTFRGRALVNTAQLQFSLHVAEGME 341
 DB 241 KMCHENLVRLGLYLHOGILTYMEHYSKGNLVNLTFRGRALVNTAQLQFSLHVAEGME 300
 QY 342 YLESKLVHRDLAARNILVSEDLVAVKVSDFGLAKAERKGLDSSRLPYKWTAPALKHGF 401
 DB 301 YLESKLVHRDLAARNILVSEDLVAVKVSDFGLAKAERKGLDSSRLPYKWTAPALKHGF 360
 QY 402 TSKSDVWSPFGLLMEVFSYGRAPYPKMSLKEVSEAVKGRMPPECGPPIVHLMSSCW 461
 DB 361 TSKSDVWSPFGLLMEVFSYGRAPYPKMSLKEVSEAVKGRMPPECGPPIVHLMSSCW 420
 QY 462 EAPRRPRPRKLAELKARELSAGAPASVSGODADGSTSPRSQEP 507
 DB 421 EAPRRPRPRKLAELKARELSAGAPASVSGODADGSTSPRSQEP 466

RESULT 5
 AAM64454
 ID AAM64454 standard; Protein; 528 AA.
 XX
 AC AAM64454;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Human matk protein.
 XX
 KW Breast; cancer; matk; CSK homologous kinase; CHK; detection; diagnosis;
 KW cytoplasmic protein; tyrosine kinase; ErbB-2; negative regulator;
 KW mitogenic signalling.
 XX
 OS Homo sapiens.
 XX
 PN MO9830704-A1.
 XX
 PD 16-JUL-1998.
 XX
 PF 07-JAN-1998; 98MO-US00420.
 XX
 PR 16-JUN-1997; 97US-0876882.

PR 08-JAN-1997; 97US-0035228.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Avraham H, Groopman JE;
 XX
 DR WPI; 1998-399149/34.
 XX
 DR N-PSDB; AAV44497.
 XX
 PT Detecting breast cancer by detecting Csk homologous kinase
 PT expression - especially in humans and use of Csk homologous kinase
 PT in treatment or prophylaxis of breast cancer and for producing
 PT medicaments
 PS
 PS Disclosure; Fig 2; 54pp; English.
 XX
 CC This sequence represents a CSK homologous kinase (CHK) which is used in a
 CC method of detecting cancer in breast tissue. The method allows diagnosis
 CC of breast cancer in mammals, especially humans. It is based on the
 CC discovery that a cytoplasmic protein tyrosine kinase, CHK, is expressed
 CC in human breast tissue, but not in adjacent tissue. This protein can be
 CC used to raise antibodies which can be included in compositions and
 CC diagnostic kits for diagnosis of breast cancer. The presence of CHK in
 CC breast tissue can also be determined using other standard methods (e.g.
 CC Northern blotting) or by detecting nucleic acid sequences encoding all/a
 CC portion of the protein (e.g. using hybridisation probes). Over-expression
 CC of the receptor tyrosine kinase ErbB-2 has previously been associated
 CC with the development of breast cancer, and CHK specifically interacts
 CC with activated ErbB-2, and may function as a negative regulator of
 CC ErbB-2 mediated mitogenic signalling. The compositions may also be used
 CC to design drugs (e.g. which incorporate CHK analogues with greater
 CC biological activity than CHK) and to identify CHK antagonists and
 CC agonists for therapeutic use.
 CC
 SO Sequence 528 AA:

Query Match 91.1%; Score 2434.5; DB 19; Length 528;
 Best Local Similarity 93.3%; Pred. No. 1.5e-219;
 Matches 472; Conservative 1; Mismatches 18; Indels 15; Gaps 3;

QY 1 MAGRGSIVSWRAFHGDSAEFLPRVSPRLRAHPPVSAKMTPTRRAPGTCITCEHT 60
 DB 1 MAGRGSIVSWRAFHGDSAEFLPRVSPRLRAHPPVSAKMTPTRRAPGTCITCEHT 60
 QY 61 RPKPGELAFKRGDVTITLACENKSWYKVNHTSGOGLLAAGALRERALSADPKLSL 119
 DB 61 RPKPGELAFKRGDVTITLACENKSWYKVNHTSGOGLLAAGALRERALSADPKLSL 120
 QY 120 MPWFHKGISGOEAVOOLPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRYLHRDGLHT 179
 DB 121 MPWFHKGISGOEAVOOLPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRYLHRDGLHT 180
 QY 180 IDEAVFPCNLMDVHEHYSKDKGALCTKLVRPRKHKGTSAEELARAGMLNLQHLTTGA 239
 DB 181 IDEAVFPCNLMDVHEHYSKDKGALCTKLVRPRKHKGTSAEELARAGMLNLQHLTTGA 240
 QY 240 QIGEGEFGAVLOGEYLGQVAVKNIKCDVTAQAFIDEAVMTKMCHENLVRLGLYLHOG 299
 DB 241 QIGEGEFGAVLOGEYLGQVAVKNIKCDVTAQAFIDEAVMTKMCHENLVRLGLYLHOG 300
 QY 300 LYTYMEHYSKGNLVNLTFRGRALVNTAQLQFSLHVAEGMEYLESKLVHRDLAARNIL 359
 DB 301 LYTYMEHYSKGNLVNLTFRGRALVNTAQLQFSLHVAEGMEYLESKLVHRDLAARNIL 360
 QY 360 VSEDVLAAYSDPGLAERKGLDSSRLPYKWTAPALKHGFPSKSDVWSPFGLLMEVFS 419
 DB 361 VSEDVLAAYSDPGLAERKGLDSSRLPYKWTAPALKHGF-FTSKSDVWSPFGLLMEVFS 419
 QY 420 YGRAPYPKMSLKEVSEAVKGRMPPECGPPIVHLMSSCWAEAPRRPRKLAELK 479
 DB 420 YGRAPYPKMSLKEVSEAVKGRMPPECGPPIVHLMSSCWAEAPRRPRKLAELK 479
 QY 480 RELRSAGAPASVSGODADGSTSPRSQ 505

ID	Accession	Standard	Protein	AA
Db	471	----	SANWPRSMPSGYAVGVQPPSQ	492
RESULT 6				
XX	AAU99575	standard:	Protein:	415 AA.
XX	AAU99575:			
XX	21-OCT-2002	(first entry)		
XX	Human kinase related to tyrosine kinase family.			
XX	Human; kinase; tyrosine kinase; kinase mediated disorder;			
XX	haematopoietic disorder; cell signal transduction disorder;			
XX	cancer; haemostatic; cytosstatic; enzyme.			
XX	Homo sapiens.			
XX	WO200252018-A2.			
XX	04-JUL-2002.			
XX	19-DEC-2001; 2001WO-US48546.			
XX	21-DEC-2000; 2000US-0741154.			
XX	(PEKE) PE CORP NY.			
XX	Beasley EM, Shao W, Ketchum K, Di Francesco V;			
XX	WPI; 2002-583568/62.			
XX	N-PSDB; ABK88791, ABK88792.			
XX	New isolated human kinase proteins and genes, useful in developing			
XX	drugs, as well as for diagnosing, preventing or treating disorders			
XX	associated with defective cell signal transduction, e.g. cancer or			
XX	haematopoietic disorders			
XX	Claim 1; Fig 2A; 78pp; English.			
XX	The present invention relates to the isolation of a novel human kinase			
XX	related to the tyrosine kinase family, and polynucleotide sequences			
XX	encoding it. The gene encoding the kinase of the invention maps to			
XX	chromosome 19. The kinase may be used for identifying a modulator of			
XX	the kinase, an agent that binds to the kinase, or for identifying			
XX	other members of the family. The kinase may also be used to raise			
XX	antibodies which may be used in immunoassays or drug screening assays.			
XX	The sequences of the invention may be used for treating a disease or			
XX	condition mediated by a human kinase such as haematopoietic disorders			
XX	and other disorders associated with defective cell signal transduction			
XX	(e.g. cancer). The polynucleotide sequences encoding the kinase are			
XX	useful for isolating and purifying the kinase, and as probes or primers.			
XX	The present sequence represents the human kinase of the invention.			
XX	Sequence 415 AA:			
XX	Query Match 75.3%; Score 2012; DB 23; Length 415;			
XX	Best Local Similarity 100.0%; Pred. No. 5e-180;			
XX	Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
Qy	122 WFNKRSQEAVALQDPEDGFLFVRESARHNGDVLVCSFGRDVIHYRVLRHROGLTLD	181		
Db	30 WFNKRSQEAVALQDPEDGFLFVRESARHNGDVLVCSFGRDVIHYRVLRHROGLTLD	89		
Qy	182 EAVFECNLMQVNEHYSKDKGAICTKLVPRKRKGTSAEELARAGWLINTLQHLTGAQI	241		
Db	90 EAVFECNLMQVNEHYSKDKGAICTKLVPRKRKGTSAEELARAGWLINTLQHLTGAQI	149		
Qy	242 GEGEGAVLQEGEYLQAKVAVNKKCDVTAQAFLDETAVTMKQKHENVLYLLGVLHOGLY	301		
Db	150 GEGEGAVLQEGEYLQAKVAVNKKCDVTAQAFLDETAVTMKQKHENVLYLLGVLHOGLY	209		

QY	302	IVMEHVSNGNIVNPELRTGRLALVNTAOLQSLHVAEEMVEYSESKLVHRDLAANNILVS	361
Db	210	IVMEHVSNGNIVNPELRTGRLALVNTAOLQSLHVAEEMVEYSESKLVHRDLAANNILVS	269
QY	362	EDLVAKVSDFGILAKAKERRGGLDSSRLPVKMTAPEALKHGKFTSKSDVMSFGVLLMVEFSYG	421
Db	270	EDLVAKVSDFGILAKAKERRGGLDSSRLPVKMTAPEALKHGKFTSKSDVMSFGVLLMVEFSYG	329
QY	422	RAPYPKMSLKEVSEAVEKGYRMEPPEGCPGVHVLMSSCWEAEAPARRPPFKLAEKLARE	481
Db	330	RAPYPKMSLKEVSEAVEKGYRMEPPEGCPGVHVLMSSCWEAEAPARRPPFKLAEKLARE	389
QY	482	LRSGAPASVSGODADGSTSPRSOEP	507
Db	390	LRSGAPASVSGODADGSTSPRSOEP	415
RESULT 7			
ID	AA71131	standard. Protein; 246 AA.	
XX	AA71131;		
AC			
XX			
XX	25-MAR-2003 (updated)		
DT	27-OCT-1995 (first entry)		
DE	Tyrosine kinase domain of cytoplasmic tyrosine kinase.		
XX			
XX	cytoplasmic; tyrosine kinase; blood; cell differentiation;		
KW	screening; anticancer agent.		
XX			
OS	Homo sapiens.		
XX			
XX	WO9506113-A1.		
PN			
PD	02-MAR-1995.		
XX			
PP	25-AUG-1994; 94WO-JP01411.		
XX			
XX	25-AUG-1993; 93JP-0210403.		
PR	29-MAR-1994; 94JP-0058553.		
XX			
PA	(ASAH) ASAH KASEI KOGYO KK.		
XX			
PI	Sakano S;		
XX			
XX	WPI; 1995-106842/14.		
DR	N-PSDB; AAO84888.		
XX			
PT	Cytoplasmic tyrosine kinase and antibody recognising it - for		
PP	screening chemical substances for tyrosine kinase inhibitory or		
PP	activating activity for use as cancer therapy		
XX			
PS	Claim 1; Page 39; 58pp; English.		
XX			
CC	A cytoplasmic tyrosine kinase which has enhanced expression in		
CC	connection with blood cell differentiation has been isolated from the		
CC	human UT-7 blood cell line. This sequence comprises the tyrosine		
CC	kinase domain of the enzyme (residues 192-437of AAR71132; residues		
CC	233-478 of AAR71133). The DNA sequences and antibodies raised against		
CC	the enzyme, are useful for screening agents for inhibiting or activating		
CC	activity on the tyrosine kinase, for use as anticancer agents.		
CC	(Updated on 25-MAR-2003 to correct PN field.)		
XX			
XX	Sequence 246 AA;		
Query Match	47.2%;	Score 1261;	DB 16; Length 246;
Best Local Similarity	99.6%;	Pred. No. 7.9e-110;	
Matches 245;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
QY	QHLTLGAQIGGEFGAVLQGEYLGQKAVVKNIKCDVTQAQFLDETAVMTKQOHENLVRL	292	

Db 1 OHLTGLGAQIGEGFAGVLAQGEYLGQKVAANKIKCDVTAQAFLEDTAVMTKQHEHENVLL 60
QY 293 GVILHOGILYIMEHVSNGNLVNFRTGRALVNTAQLLOPSLAHAEEMYLESKLYHRD 352
Db 61 GVILHOGILYIMEHVSNGNLVNFRTGRALVNTAQLLOPSLAHAEEMYLESKLYHRD 120
QY 353 LAARNILVSEDLVAKVSDPGLAKAERKGLDSSRLPVKWTAPALAKHGKFTSKSDVMSFGV 412
Db 121 LAARNILVSEDLVAKVSDPGLAKAERKGLDSSRLPVKWTAPALAKHGKFTSKSDVMSFGV 180
QY 413 LIMEVSEYGRAPYKMSLKEVSEAVEKGRPEPGCGPVHVLMSCEMEAPRRPPFR 472
Db 181 LIMEVSEYGRAPYKMSLKEVSEAVEKGRPEPGCGPVHVLMSCEMEAPRRPPFR 240
QY 473 KIAEKL 478
Db 241 KIAEKL 246
RESULT 8
AAO13873 standard; Protein: 459 AA.
XX AAO13873;
AC AAO13873;
DF 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 27765.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
XX 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
XX
DR N-PSDB; AAI93804.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20: SEQ ID NO 27765; 1399bp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 459 AA;
Query Match 46.7%; Score 1247.5; DB 22; Length 459;
Best Local Similarity 53.2%; Pred. No. 3.7e-108;
Matches 238; Conservative 82; Mismatches 118; Indels 9; Gaps 3;
QY 40 ARMPTR-----RWAPGTQCITKCEHTPRKPGELAFKRGDVVTILECENKSWRYKHHHT 93
Db 4 ARAPKMSAIOAMPSCSTECIAKYNFNGTAEOQLPFCQGDVLTIVATKDPNNYKAKNKV 63
QY 94 SGOEGLLAALAKERALSADPKLSLMPWHGKISGOEAVQOQLPPEDGFLYRESARHP 153
Db 64 -GREGIIPANYVOKREGVKAGTKLSLMPWHGKITRQARLLYPPETGLFLVRESSTNP 122
QY 154 GDYVLCYSFGRDVIHYHVLNRDGLTIDEAVFFCNLMQVNEHYSKDKGATCTKLVPRRK 213
Db 123 GDYTLVCSCDCKGKVEHRYIMHASKLSIDEVYVENLMQVNEHYSKDKGATCTKLVPRRK 182
QY 214 HGTKSAEELARAGWLINLOHLTGLGAQIGEGFAGVLAQGEYLGQKVAANKIKCDVTAQAF 273
Db 183 EGTVAADDEFYRSGMALNMRKELKLTQIGKGEFGDVMLGDRGNKVAVKCIKNDATAQAF 242
QY 274 LDETAVMTKQHEHENVLLGLVLIHQ--GLYIYMEHVSNGNLVNFRTGRALVNTAQLLO 331
Db 243 LAEASVMTQLRHSNLVQLGLVIEKGLYIYMEHVSNGNLVNFRTGRALVNTAQLLO 302
QY 332 FSLHVAEGMEYLESKLYHRDLAARNILVSEDLVAKVSDPGLAKAERKGLDSSRLPVKWT 391
Db 303 FSLDVCCEAMEYLEGNNNFVHRDLAARNILVSEDLVAKVSDPGLAKAERKGLDSSRLPVKWT 362
QY 392 APEALKHGKFTSKSDVMSFGVLMVEVSYGRAPYKMSLKEVSEAVEKGRPEPGCG 451
Db 363 APEALREKFKSTSDVMSFGVLMVEVSYGRAPYKMSLKEVSEAVEKGRPEPGCG 422
QY 452 PVHVLMSCEMEAPRRPPRKLAEKL 478
Db 423 AYTEVMKNCWHLDAAMPSTLQLEOL 449
RESULT 9
AAV44448 standard; Protein: 450 AA.
XX AAV44448;
AC AAV44448;
DF 22-MAR-2000 (first entry)
XX
DE Wild-type human c-Src tyrosine kinase.
XX
KW Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
KW human; viral expression vector; replication competent; mutant Src;
KW inflammatory disease; arthritis; rheumatoid arthritis; restenosis;
KW diabetic retinopathy; osteoporosis; cancer.
XX
OS Homo sapiens.
XX
PN WO9961590-A1.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11780.
XX
PR 29-MAY-1998; 98US-0087220.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Cheresah DA, Eliceiri B, Schwartzberg PL;
XX
DR WPI; 2000-116335/10.
XX
DR N-PSDB; AAZ29701.
XX
PT Using tyrosine kinase Src for modulating angiogenesis in tissues useful
PT in, e.g. treatment of chronic articular rheumatism -

XX Claim 1, Fig 4; 80pp; English.

PS The present sequence is the wild-type human c-Src tyrosine kinase. This

XX CC Src protein can be used to modulate angiogenesis. When the Src protein

CC is inactivated, angiogenesis is inhibited, while when it is activated,

CC angiogenesis is potentiated. The modified or variant Src can be used to

CC treat inflammatory diseases like arthritis, rheumatoid arthritis,

CC diabetic retinopathy, restenosis, osteoporosis and cancer associated

CC disorders.

XX Sequence 450 AA;

SQ

Query Match 46.6%; Score 1245.5; DB 21; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.5e-108; Indels 3; Gaps 2;

Matches 235; Conservative 81; Mismatches 115;

QY 47 WAPGTCITKCEHTRPKGLAFKRGDVTITLACENKSMYRKHNHSGOGLIAGALR 106

DB 8 WPGSTECIAKYNFHGTAEODLPFCCKGDVLTIVATKDPNMYKAKNKV-GREGIIPANYQ 66

QY 107 EREALSDAPKLSIMPWFHKGISGOEAVQOLQPPEDGLFLVRESARHPGDVLCVSGRDY 166

DB 67 KREGVKAGTKLSIMPWFHKGITREQAERLLYPETGLFLVRESYTPGDYTLVSCDGKY 126

QY 167 IHRYVLHRDGLHTIDEAVFCNLMDMVEHYSKDKGALCTKLVPRKRHGRKSAEELARA 226

DB 127 EHRIMHASKLSIDEVEYFENLMQVLEHTSDAGLCTLRKPKWEGTVAODEFYRS 186

QY 227 GWLINTLOHTLGAOIGEGEFAVLQGEYLQKAVKNIKCDVTAQAFLDETAVTQKQHE 286

DB 187 GWLNMKELKLTQIGKEFGDVMLDYRGKNKVAKCICKNDATAQAFLAASVVTQLRHS 246

QY 287 NLVRLGVIIHQ--GLYIVMEHYSKGLVNFRLRGALVNTAQLQFSLHVAEGMYLE 344

DB 247 NLVOLLGVIIEEKGLIVTEYMAKGLVDYLSRSGSVLGGDCLLKFSLDVEAMYLE 306

QY 345 SKKLVHDLAARNILVSEDLVAKVSDGLKAERKGDSSRLPKVTPAPALKHGRPTSK 404

DB 307 GNNFVHDLAARNVIVSEDNVAKVSDGLTKKEASTDQTLKPLKVPAPALKRKRSTK 366

QY 405 SDVMSFGVLLMEVFSIGRADYPKMSLKEVSEAVEKGRMEPPGCGPVHVLSSCWEAE 464

DB 367 SDVMSFGILLMEIYSFGRVYPRIPLKDVVPREKGYKMDAPDCCPRAVEVMKNCWHL 426

QY 465 PARPPPRKLAETL 478

DB 427 AAMPSPFLQREOL 440

RESULT 10

ID AAY49418 standard; Protein; 450 AA.

XX AAY49418;

AC

XX 13-MAR-2000 (first entry)

DE PKA substrate, Csk-family protein.

XX

KM Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;

KM kinase substrate; immunosuppressive disorder; proliferative disease;

KM HIV infection; AIDS; immunodeficiency; autoimmune disease; Chk; Lsk; Hyl;

KM systemic lupus erythematosus; Csk-family; Matk; Ctk; Btk; Ntk.

XX Homo sapiens.

OS

XX WO9962315-A2.

PN

XX 02-DEC-1999.

PD

XX 27-MAY-1999; 99WO-GB01680.

XX

PR 27-MAY-1998; 98NO-0002419.

PR 30-DEC-1998; 98US-0114240.

XX (LAUR-) LAURAS AS.

PA (JONE/) JONES E L.

XX

PI Hansson V, Levy FO, Mustelin T, Skalhogg BS, Sundvoid V, Tasken K;

PI Vang T, Altman A, Munshi A;

XX WPI; 2000-086801/07.

DR N-PSDB; AAZ46489.

XX

PT Altering the activity of protein kinase signaling pathways, used for

PT treating immunosuppressive disorders, e.g. AIDS, proliferative

PT disorders, e.g. cancers or autoimmune diseases

PS Claim 12; Page 89-90; 111pp; English.

XX

CC The invention provides a novel method of altering the activity of the

CC protein kinase A (PKA) signaling pathway in a cell that comprises

CC altering the extent of phosphorylation of one or more PKA substrates, or

CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical

CC compositions containing a nucleic acid molecule that encodes a PKA

CC substrate, or fragment, precursor or functionally equivalent variant,

CC where the sequence is modified to alter its susceptibility to

CC phosphorylation by PKA can be used for treating a disorder exhibiting

CC abnormal PKA signaling activity, immunosuppressive disorders or

CC proliferative diseases. They can be used for treating e.g. HIV

CC infection, AIDS, common variable immunodeficiency or cancers. Conditions

CC in which upregulation of the PKA pathway is required, such as autoimmune

CC disease, e.g. systemic lupus erythematosus, may also be treated. The

CC present sequence represents a PKA substrate, wherein the substrate is in

CC the Csk-family, preferably Csk, Chk, Lsk, Hyl, Matk, Ctk, Btk or Ntk.

XX

SQ Sequence 450 AA;

Query Match 46.6%; Score 1245.5; DB 21; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.5e-108;

Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

QY 47 WAPGTCITKCEHTRPKGLAFKRGDVTITLACENKSMYRKHNHSGOGLIAGALR 106

DB 8 WPGSTECIAKYNFHGTAEODLPFCCKGDVLTIVATKDPNMYKAKNKV-GREGIIPANYQ 66

QY 107 EREALSDAPKLSIMPWFHKGISGOEAVQOLQPPEDGLFLVRESARHPGDVLCVSGRDY 166

DB 67 KREGVKAGTKLSIMPWFHKGITREQAERLLYPETGLFLVRESYTPGDYTLVSCDGKY 126

QY 167 IHRYVLHRDGLHTIDEAVFCNLMDMVEHYSKDKGALCTKLVPRKRHGRKSAEELARA 226

DB 127 EHRIMHASKLSIDEVEYFENLMQVLEHTSDAGLCTLRKPKWEGTVAODEFYRS 186

QY 227 GWLINTLOHTLGAOIGEGEFAVLQGEYLQKAVKNIKCDVTAQAFLDETAVTQKQHE 286

DB 187 GWLNMKELKLTQIGKEFGDVMLDYRGKNKVAKCICKNDATAQAFLAASVVTQLRHS 246

QY 287 NLVRLGVIIHQ--GLYIVMEHYSKGLVNFRLRGALVNTAQLQFSLHVAEGMYLE 344

DB 247 NLVOLLGVIIEEKGLIVTEYMAKGLVDYLSRSGSVLGGDCLLKFSLDVEAMYLE 306

QY 345 SKKLVHDLAARNILVSEDLVAKVSDGLKAERKGDSSRLPKVTPAPALKHGRPTSK 404

DB 307 GNNFVHDLAARNVIVSEDNVAKVSDGLTKKEASTDQTLKPLKVPAPALKRKRSTK 366

QY 405 SDVMSFGVLLMEVFSIGRADYPKMSLKEVSEAVEKGRMEPPGCGPVHVLSSCWEAE 464

DB 367 SDVMSFGILLMEIYSFGRVYPRIPLKDVVPREKGYKMDAPDCCPRAVEVMKNCWHL 426

QY 465 PARPPPRKLAETL 478

DB 427 AAMPSPFLQREOL 440

```

RESULT 11
AAB84662
ID AAB84662 standard; Protein; 450 AA.
XX
AC AAB84662;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of human tyrosine kinase protein Src.
XX
KM Vascular permeability; tyrosine kinase protein; Src; Yes; stroke;
KM myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis;
KM diabetic retinopathy; inflammatory disease; infection; arthritis;
KM adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KM diabetic retinopathy; psoriasis; neovascular glaucoma;
KM capillary proliferation; osteoporosis; cancer.
XX
XX Homo sapiens.
XX
XX WO200145751-A1.
XX
XX 28-JUN-2001.
XX
XX 22-DEC-2000; 2000MO-US35396.
XX
XX 22-DEC-1999; 9905-0470881.
XX
XX 29-MAR-2000; 2000US-0538248.
XX
XX (SCRI) SCRIpps RES INST.
XX
XX Cheresch DA, Eliceiri B, Paul R;
XX
XX WPI: 2001-417982/44.
XX
XX N-PSDB; AAH28358.
XX
XX Modulating vascular permeability in tissues, including inflamed tissue,
XX tissues associated with stroke, myocardial infarction, by contacting
XX the tissue with tyrosine kinase protein Src, Yes or their modified
XX forms.
XX
XX Disclosure; Fig 4; 133pp; English.
XX
XX PS The specification describes a method for modulating vascular
XX permeability in a tissue suffering from a disease condition. The method
XX comprises contacting the tissue with a pharmaceutical composition
XX comprising tyrosine kinase protein Src, Yes or their mixtures or
XX nucleic acid expressing them. The method is useful for modulating
XX vascular permeability in tissues, including inflamed tissue, tissues
XX associated with stroke, myocardial infarction or other blockage of
XX normal flow, tissues undergoing restenosis, psoriatic, retinal tissue
XX and similar tissues. Pathologies which may be treated include
XX trauma to blood vessels, and other systemic pathological events such as
XX atherosclerosis, diabetic retinopathy, inflammatory disease due to
XX infection by microbial agents and arthritis. Other diseases which can
XX be treated include adult respiratory distress syndrome (ARDS), rheumatoid
XX arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma,
XX capillary proliferation in atherosclerotic plaques and osteoporosis and.
XX cancer associated disorders such as solid tumours, solid tumour
XX metastases, angiofibromas and hemangiomas. The present sequence
XX represents human Src, and is used in the method of the invention.
XX
XX SQ Sequence 450 AA;
XX
XX Query Match 46.6%; Score 1245.5; DB 22; Length 450;
XX Best Local Similarity 54.1%; Pred. No. 5.5e-108;
XX Matches 225; Conservative 81; Mismatches 115; Indels 3; Gaps 2;
XX
XX 47 MARGTCTRCCEHTRRKPELAFRKGDVYITLACENKSMYRKVHTTSGOGLAAGALR 106
XX | | | | | : | | | | | : : | | | : | | | | : :
XX 8 WPGGTGCIKYNHFGAEDDLPKCKGDVLTIVAVTDPMMYKAKNV-GREGIIPANYVQ 66
XX | | | | | : | | | | | : : | | | : | | | | : :
XX 107 ERRAALSADRLSLMPFHGKISQGEAVOOLQPPEDCLFLVRSARHPGDVILCVSFGROV 166
XX | | | | | : | | | | | : : | | | : | | | | : :

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```

DB 67 KREGVAGTKLSLMPFHGKITREQAERLLYPETGLFLVRESTNYPGDYTLVCSCDGK 126
QY 167 IHRVRLHRDGHLLIDEAVFECNLMQVHEHYSKDKAICIKLVPRKRHGTGAEELARA 226
| | | | | : | | | | | : | | | | | : | | | | | :
DB 127 EHRIRVYHASKLSLIDEVYFENLMQVHEHTSDAGICTRLIKPKVMEGTVAADDFYRS 186
QY 227 GMLNLQHLTLGAQIGEGGAVLOGEYLGQRAVANKIKCDVTAQAFIDETAVMTRMOHE 286
| | | | | : | | | | | : | | | | | : | | | | | :
DB 187 GWALNMKEIKLLOTIGKGEFQDMGLGDYGNKRVAVKCIKNDATAQAFILAEASVMQOLRHS 246
QY 287 NIVRLIGVTLHQ--GIYIMHEVSKGNLVNFTRTGRALVNTAQLLOFSLHAEGMEYLE 344
| | | | | : | | | | | : | | | | | : | | | | | :
DB 247 NVVOLLGVIEERKGLYITEYMAKGSIVDYLRSGRSVYLGDCILKESLDVCEAMEYLE 306
QY 345 SKKLVRDIAANNILVSEDLVAKVSPFGTLAKAERKGLDSSRLPVKWTAPALKHGKFTSK 404
| | | | | : | | | | | : | | | | | : | | | | | :
DB 307 GNNFVHRLDAARNVLSSENNVAKVSPFGTLKASSSTQDCKLPVMTAPALREKKFTSK 366
QY 405 SDVWSFGLLMEVFSYGRAPYPRKMSLKEVSEAVEKGRMEPPGCGPVHVLMSCEAE 464
| | | | | : | | | | | : | | | | | : | | | | | :
DB 367 SDVWSFGLLMEVFSYGRAPYPRKMSLKEVSEAVEKGRMEPPGCGPVHVLMSCEAE 426
QY 465 PARRPEPRKLAERL 478
DB 427 AAMRPSFIQLRREL 440
XX
XX RESULT 12
XX AAG67444
XX ID AAG67444 standard; Protein; 450 AA.
XX
XX AAG67444;
XX
XX 26-NOV-2001 (first entry)
XX
XX Amino acid sequence of a human polypeptide.
XX
XX DE Human; protein kinase; protein phosphatase; signal transduction;
XX intracellular signalling pathway.
XX
XX KM Homo sapiens.
XX
XX OS
XX
XX XX WO200109345-A1.
XX
XX 08-FEB-2001.
XX
XX PF 28-JUL-2000; 2000MO-JP05060.
XX
XX PR 29-JUL-1999; 99JP-0248036.
XX
XX PR 18-OCT-1999; 9905-0159590.
XX
XX PR 11-JAN-2000; 2000JP-0118776.
XX
XX PR 17-FEB-2000; 2000US-0183322.
XX
XX PR 02-MAY-2000; 2000JP-0183767.
XX
XX PA (HELI-) HELIX RES INST.
XX
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
XX Seno C, Nezu J;
XX
XX DR WPI: 2001-564736/63.
XX
XX PT New genes encoding protein kinase and protein phosphatase, useful for
XX identifying modulators which can be used to treat human or animal
XX disorders associated with the expression or function of these enzymes -
XX
XX PS Example 4; Page 249-252; 336pp; Japanese.
XX
XX The specification describes human protein kinase/protein phosphatases.
XX The polypeptides are expected to participate in signal transduction
XX in cells. The kinase phosphatases are connected with intracellular
XX signalling pathways. Antisense oligonucleotides and compounds
XX identified by screening (agonists or antagonists) can be used to

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CC treat human or animal disorders associated with the expression
CC or function of the protein. In addition, the polypeptides may be used
CC as target molecules for drug development. The present sequence
CC represents a polypeptide, used in the course of the invention.

XX Sequence 450 AA;

Query Match 46.6%; Score 1245.5; DB 22; Length 450;
Best Local Similarity 54.1%; Pred. No. 5.5e-108;
Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

OY 47 WAPGTCITCKEHTPRKPGELAFKRGDVTLLAECKNSWYRVKHHSTGQGLAAGLR 106
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 8 WPSGTECIKAKNFHGTABDLPFCCKGDLTVAVTKDPMWKANKKV-GREGIIPANYQ 66
OY 107 EREALSDPKISLMPWFHGTISGQEAQQLOPPEDGLFLVESARHPDYLVSFGSDV 166
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 67 KREGVKAQTKLSLMPWFHGTITREQAERLLYPPETGLFLVRESSTNYPDYTLVSCDQKV 126
OY 167 IHYVLRDHLTIDEAVFCNLMDMVHYKSKDGAICTKLYPRKRKGTSAEELARA 226
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 127 EHYRIMYHASKLSIDEVEYFENLMQVHHTSDADGLCTRLIKRKVMGTVAADDEFYRS 186
OY 227 GWLNLQHLTLGAOIGEGEFGAVLQGEYLQGVAVAKNIKCDVTAAFLDETAVMTKMOE 286
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 187 GWALNMKELKLTQITGKEFGDVMGDRGNKVAVKCIKNDATAQAFLAASVMTQLRHS 246
OY 287 NLVRLLYGVIHQ--GLTYVMEHVSNGNLYNFLRGRALVNTAQLLOFSLHVAAGMEYLE 344
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 247 NLVOLLGYIVEKGGLYIVTEYMAKGSIVDYLRSGRVSGLGDCILKFSLDVCEAMEYLE 306
OY 345 SKKLVHRDLAARNILVSEDVAKVSDGLAKAEKRGDSSRLPYKMTAPEALKHGKPTSK 404
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 307 GNNFVHRDLAARNVLSVDNNAKVSDFGLTKFEASTDPTGKLPKMTAPEALREKKSSTK 366
OY 405 SDVMSFGVLWVESYGRAPYPKMSLKEVSEAVEKGYRMEPEGCQPGVHYLMSSCWEAE 464
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 367 SDVMSFGILLWEIYSFGRVPRIPRLKDYVVRVEKGYMDAPDGPRAVYEVMMKNCWILD 426
OY 465 PARPPRPKLAEKL 478
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 427 AAMRPSFLQIREOL 440

RESULT 13

ID AAG67623 standard; Protein: 450 AA.

XX AAG67623;

DT 26-NOV-2001 (first entry)

DE Amino acid sequence of a human protein.

KW Human; protein kinase; protein phosphatase; signal transduction.

OS Homo sapiens.

XX WO200109316-A1.

PD 08-FEB-2001.

PF 28-JUL-2000; 2000WO-JP05061.

PR 29-JUL-1999; 99JP-0248036.

PR 18-OCT-1999; 99US-0159590.

PR 11-JAN-2000; 2000JP-0118776.

PR 17-FEB-2000; 2000US-0183322.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakematsu A, Nagai K, Otsuki T, Funahashi S;
PI Senoo C, Nezu J.

XX WPI: 2001-570286/64.

PT New genes encoding proteins with protein kinase/protein phosphatase
XX activity, useful in the diagnosis and treatment of diseases -
PS Example 4; Page 149-152; 233pp; Japanese.

XX The specification describes human protein kinase/protein phosphatases.
CC It is expected that the protein kinase/protein phosphatase gene
CC participates in signal transduction in cells. The protein
CC kinase/protein phosphatase polypeptides and polynucleotides are
CC useful for developing diagnostics and treatment agents for human
CC and animal diseases. The protein kinase/protein phosphatase polypeptides
CC are useful as target molecules in designing novel drugs. The protein
CC kinase/protein phosphatase polynucleotides are useful as a source of
CC probes and primers, which may be used to isolate homologous sequences.
CC The present sequence represents a human protein, which is used in the
CC course of the invention.

XX Sequence 450 AA;

Query Match 46.6%; Score 1245.5; DB 22; Length 450;
Best Local Similarity 54.1%; Pred. No. 5.5e-108;
Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

OY 47 WAPGTCITCKEHTPRKPGELAFKRGDVTLLAECKNSWYRVKHHSTGQGLAAGLR 106
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 8 WPSGTECIKAKNFHGTABDLPFCCKGDLTVAVTKDPMWKANKKV-GREGIIPANYQ 66
OY 107 EREALSDPKISLMPWFHGTISGQEAQQLOPPEDGLFLVESARHPDYLVSFGSDV 166
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 67 KREGVKAQTKLSLMPWFHGTITREQAERLLYPPETGLFLVRESSTNYPDYTLVSCDQKV 126
OY 167 IHYVLRDHLTIDEAVFCNLMDMVHYKSKDGAICTKLYPRKRKGTSAEELARA 226
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 127 EHYRIMYHASKLSIDEVEYFENLMQVHHTSDADGLCTRLIKRKVMGTVAADDEFYRS 186
OY 227 GWLNLQHLTLGAOIGEGEFGAVLQGEYLQGVAVAKNIKCDVTAAFLDETAVMTKMOE 286
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 187 GWALNMKELKLTQITGKEFGDVMGDRGNKVAVKCIKNDATAQAFLAASVMTQLRHS 246
OY 287 NLVRLLYGVIHQ--GLTYVMEHVSNGNLYNFLRGRALVNTAQLLOFSLHVAAGMEYLE 344
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 247 NLVOLLGYIVEKGGLYIVTEYMAKGSIVDYLRSGRVSGLGDCILKFSLDVCEAMEYLE 306
OY 345 SKKLVHRDLAARNILVSEDVAKVSDGLAKAEKRGDSSRLPYKMTAPEALKHGKPTSK 404
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 307 GNNFVHRDLAARNVLSVDNNAKVSDFGLTKFEASTDPTGKLPKMTAPEALREKKSSTK 366
OY 405 SDVMSFGVLWVESYGRAPYPKMSLKEVSEAVEKGYRMEPEGCQPGVHYLMSSCWEAE 464
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 367 SDVMSFGILLWEIYSFGRVPRIPRLKDYVVRVEKGYMDAPDGPRAVYEVMMKNCWILD 426
OY 465 PARPPRPKLAEKL 478
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 427 AAMRPSFLQIREOL 440

RESULT 14

ID ABR47428 standard; Protein: 450 AA.

XX ABR47428;

DT 12-JUN-2003 (first entry)

DE Breast cancer associated protein sequence SEQ ID NO:88.

KW Human; breast cancer; cytostatic; gene therapy.


```

Db      467 FPGDYTLVCVCFOSKVEHYRVAYLLENKLTIDDEEFFENLGOVLAHYEADADGICTQJIKCL 526
QY      212 RKHGTS--AEEELARAGWLLNQHLTLGAQIGSEEGANVLOGEYLGOKVAVKNKCDV 268
Db      527 PKLGKQEFJCINSKDFVDKGVIPAEIQLRESIGKEGEGDMLGILRNEKVAVMKLKDEG 586
QY      269 TQAFLDETVAMTMOHENLVRLLGVIL-HQGLYIMEHVSNGNLVNFLLPTRGRALVNTA 327
Db      587 AVQKFLAEASVMTLLEHNDLVKFIGLVFTSKHLVLYTEYMSKGSVDYLRSGRQHITTK 646
QY      328 QLOFSLHVAEGMEYLESKKLVHRDLARNLIVSEDLVAKVSDGLAKAERRGLDSSRLP 387
Db      647 DOIIFAYDTASGMETLEAKKVHRDLARNVLISEDCAKYSDFGLAREECYNLDVGKLP 706
QY      388 VKMTAPEALKHGFTSKSDVSPGVLMEVSVGRAPYPMKSLKEVSEAVEKGYRMEPE 447
Db      707 IKMTAPEALKNGRFSNKSMDMSFGILMEIISFGRVPPRLPLADVYKHAHEVGTKMEAPE 766
QY      448 GCPGPHVHLMSSCWEAEPPARRPPRKLAEKL 478
Db      767 GCPEIYEMMRQAWDLNPAKRPPTFAELKVKL 797

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Search completed: July 29, 2003, 09:50:57
 Job time : 47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2003, 09:47:52 ; Search time 16 Seconds

(without alignments)
1490.155 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671
Sequence: 1 MAGRSLVSWRAFHGDSAE.....PASVSGDADGSTRSPRSGEP 507

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2671	100.0	507	1 MATK_HUMAN	P42679 homo sapien
2	2332	87.3	505	1 MATK_MOUSE	P41242 mus musculu
3	2221.5	83.2	467	1 MATK_RAT	P41243 rattus norv
4	1253.5	46.9	450	1 CSK_CHICK	P41239 gallus gall
5	1245.5	46.6	450	1 CSK_HUMAN	P41240 homo sapien
6	1242.5	46.5	450	1 CSK_RAT	P42377 rattus norv
7	1227.5	46.0	450	1 CSK_MOUSE	P41241 mus musculu
8	762.5	28.5	507	1 LCK_CHICK	P42683 gallus gall
9	744.5	27.9	508	1 LCK_MOUSE	P06240 mus musculu
10	742.5	27.8	508	1 LCK_HUMAN	P06239 homo sapien
11	735.5	27.5	526	1 SRC_RSVP	P00524 rous sarcom
12	734.5	27.5	568	1 SRC_AVISR	P14084 avian sarco
13	734	27.5	557	1 SRC_AVISR	P14085 avian sarco
14	733	27.4	532	1 SRC_CHICK	P00523 gallus gall
15	731.5	27.4	526	1 SRC_AVISR	P00525 avian sarco
16	731.5	27.4	587	1 SRC_AVIS2	P15054 avian sarco
17	727.5	27.2	523	1 SRC_RSVP	P31693 rous sarcom
18	727	27.2	535	1 SRC_HUMAN	P12931 homo sapien
19	726	27.2	531	1 SRC1_XENLA	P13115 xenopus lae
20	724.5	27.1	526	1 HCK_HUMAN	P08631 homo sapien
21	724.5	27.1	526	1 SRC_RSVP	P25020 rous sarcom
22	724	27.1	531	1 SRC2_XENLA	P13116 xenopus lae
23	724	27.1	1520	1 ABL_DROME	P00522 drosophila
24	723.5	27.1	526	1 SRC_RSVP	P00526 rous sarcom
25	716.5	26.8	535	1 SRC_RAT	P2666 rattus norv
26	716	26.8	505	1 SRC1_SPOLA	P2666 rattus norv
27	714	26.7	540	1 SRC_MOUSE	P05480 mus musculu
28	713	26.7	506	1 SRC4_SPOLA	P42690 spongilla l
29	713	26.7	511	1 LYX_RAT	P07014 rattus norv
30	710	26.6	541	1 YES_MOUSE	P04736 mus musculu
31	710	26.6	543	1 YES_HUMAN	P07947 homo sapien
32	709	26.5	536	1 FYN_XIPHE	P27446 xiphophorus
33	707	26.5	504	1 HCK_MACPA	G95m30 macaca fasc

34	707	26.5	511	1 LYX_HUMAN	P07948 homo sapien
35	706.5	26.5	524	1 HCK_MOUSE	P08103 mus musculu
36	706	26.4	511	1 LYX_MOUSE	P25911 mus musculu
37	706	26.4	541	1 YES_CHICK	P09324 gallus gall
38	705	26.4	544	1 YES_XIPHE	P27447 xiphophorus
39	700.5	26.2	503	1 HCK_RAT	P50543 rattus norv
40	700	26.2	537	1 YES_XENLA	P10936 xenopus lae
41	699.5	26.2	535	1 YRK_CHICK	P02977 gallus gall
42	699	26.2	498	1 BLK_MOUSE	P16277 mus musculu
43	699	26.2	822	1 PER_HUMAN	P16591 homo sapien
44	698.5	26.2	536	1 FYN_HUMAN	P06241 homo sapien
45	698.5	26.2	536	1 FYN_XENLA	P13406 xenopus lae

ALIGNMENTS

RESULT 1	ID	MATK_HUMAN	STANDARD	PRT	507 AA.
AC	P42679;				
DT	01-NOV-1995 (Rel. 32, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112)				
DE	(tyrosine-protein kinase CTK) (Protein kinase HYL) (Hematopoietic				
DE	consensus tyrosine-lacking kinase).				
GN	MATK OR CTK OR HYL.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RX	SEQUENCE FROM N.A.				
RA	MEDLINE=94181267; PubMed=8134117;				
RA	Sakano S., Iwama A., Inazawa J., Ariyama T., Ohno M., Suda T.;				
RT	"Molecular cloning of a novel non-receptor tyrosine kinase, HYL				
RT	(hematopoietic consensus tyrosine-lacking kinase).";				
RL	Oncogene 9:1155-1161(1994).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Megakaryocytes;				
RX	MEDLINE=94117408; PubMed=8288563;				
RA	Bennett B.D., Cowley S., Jiang S., London R., Deng B., Grabarek J.,				
RA	Groopman J.E., Goeddel D.V., Avraham H.;				
RT	"Identification and characterization of a novel tyrosine kinase from				
RT	megakaryocytes.";				
RL	J. Biol. Chem. 269:1068-1074(1994).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95130565; PubMed=7530249;				
RA	Avraham S., Jiang S., Ota S., Fu Y., Deng B., Dowler L.L.,				
RA	White R.A., Avraham H.;				
RT	"Structural and functional studies of the intracellular tyrosine				
RT	kinase MATK gene and its translated product.";				
RL	J. Biol. Chem. 270:1833-1842(1995).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RP	Lamerdin J.E., McGready P.M., Skowronski E., Viswanathan V.,				
RA	Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,				
RA	Pahn H., Velasco N., De L., Regala W., Terry A., Ganes J.,				
RA	Dangnan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,				
RA	Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,				
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,				
RA	Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,				
RL	Olsen A.S., Carrara A.V.;				
RL	Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Eye;				
RX	MEDLINE=22488257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				

RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
RA Valliano D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Bialesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallus D.E.,
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [6]
RP CHARACTERIZATION.
RX MEDLINE:95022650; PubMed:7936664;
RA Hamauchi I., Iwama A., Yamauchi N., Sakano S., Matsuda Y., Suda T.,
RT "Characterization of mouse non-receptor tyrosine kinase gene, HTL.",
RL Oncogene 9:3371-3374(1994).
CC -1- FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION
CC OF HEMATOPOIETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF
CC SRC-FAMILY MEMBERS IN BRAIN BY SPECIFICALLY PHOSPHORYLATING THEIR
CC C-TERMINAL REGULATORY TYROSINE RESIDUE WHICH ACTS AS A NEGATIVE
CC REGULATORY SITE. IT MAY PLAY AN INHIBITORY ROLE IN THE CONTROL OF
CC T-CELL PROLIFERATION.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS MYELOID CELL LINES,
CC DETECTED IN BRAIN AND LUNG.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC -----
DR EMBL: L18974; AAA16703.1; -;
DR EMBL: X77278; CA54493.1; -;
DR EMBL: S75168; AAC60645.1; -;
DR EMBL: S75145; AAC60645.1; JOINED.
DR EMBL: S75147; AAC60645.1; JOINED.
DR EMBL: S75166; AAC60645.1; JOINED.
DR EMBL: S75151; AAC60645.1; JOINED.
DR EMBL: S75153; AAC60645.1; JOINED.
DR EMBL: S75155; AAC60645.1; JOINED.
DR EMBL: S75156; AAC60645.1; JOINED.
DR EMBL: S75158; AAC60645.1; JOINED.
DR EMBL: S75159; AAC60645.1; JOINED.
DR EMBL: S75162; AAC60645.1; JOINED.
DR EMBL: S75164; AAC60645.1; JOINED.
DR EMBL: AC005277; AAC62843.1; -;
DR EMBL: BC000114; AAH00114.1; -;
DR PIR: A49865; A49865.
DR PIR: A53625; A53625.
DR PDB: 1JWO; 12-SEP-01.
DR GeneW: HGNC:6906; MATH.
DR MIM: 600038; -;
DR GO: GO:0005515; F:protein binding activity; TAS.
DR GO: GO:0004713; F:protein tyrosine kinase activity; TAS.
DR GO: GO:0008283; P:cell proliferation; TAS.
DR GO: GO:0007498; P:mesoderm development; TAS.

DR	GO:	GO:0008284;	P:positive regulation of cell proliferation; TAS.
DR	GO:	GO:0006468;	P:protein amino acid phosphorylation; TAS.
DR	GO:	GO:0000074;	P:regulation of cell cycle; TAS.
DR	InterPro:	IPIR000719;	Prot_kinase.
DR	InterPro:	IPIR000980;	SH2.
DR	InterPro:	IPIR001452;	SH3.
DR	InterPro:	IPIR001245;	Tyr_kinase.
DR	pfam:	PF000069;	kinase; 1.
DR	pfam:	PF000017;	SH2; 1.
DR	pfam:	PF000018;	SH3; 1.
DR	PRINTS:	PR00401;	SH2DOMAIN.
DR	PRINTS:	PR00109;	TYRKINASE.
DR	ProDom:	PD0000001;	Prot_kinase; 1.
DR	ProDom:	PD000093;	SH2; 1.
DR	SMART:	SMO0252;	SH2; 1.
DR	SMART:	SMO0326;	SH3; 1.
DR	SMART:	SMO0219;	TyrcKc; 1.
DR	PROSITE:	PS00107;	PROTEIN_KINASE_ATP; 1.
DR	PROSITE:	PS00109;	PROTEIN_KINASE_TYR; 1.
DR	PROSITE:	PS50011;	PROTEIN_KINASE_DOM; 1.
DR	PROSITE:	PS50002;	SH3; 1.
DR	Transferrase:		Tyrosine-protein kinase; ATP-binding; SH2 domain;
KM	SH3 domain:		Phosphorylation; 3D-structure.
FT	DOMAIN	58	110
FT	DOMAIN	122	211
FT	NP_BIND	235	482
FT	BINDING	241	249
FT	ACT_SITE	352	352
FT	CONFLICT	107	108
FT	CONFLICT	400	400
FT	CONFLICT	466	507
SO	SEQUENCE	507 AA;	56469 MW; 8572106E04575EF CRC64;
	Query Match	Best Local Similarity	100.0%; Score 2671; DB 1; Length 507;
	Matches	507; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1	MAGRSLSVSWRAFHHCDCSAEELPRVSPREFLRMHPPVSARMPTRMAAPGTCITRCHEHT	60
DB	1	MAGRSLYSWRAFHHCDCSAEELPRVSPREFLRMHPPVSARMPTRMAAPGTCITRCHEHT	60
OY	61	RPKPGELAFRKGDDVTTLLEACENKSWRYVKNNHTSGQEGLLAAGALREREALSADRPXLSIM	120
DB	61	RPKPGELAFRRKGDDVTTLLEACENKSWRYVKNNHTSGQEGLLAAGALREREALSADRPXLSIM	120
OY	121	PMFHGKISGORAVVOQLDPEDGLFLVRESARRPGDYVLCSGRGVNIHYRVLHRGHILTI	180
DB	121	PMFHGKISGORAVVOQLDPEDGLFLVRESARRPGDYVLCSGGRVNIHYRVLHRGHILTI	180
OY	181	DEAVFCMLDMVMVEHYSKDGCATCTKLVRPKRHGTKSAEEELARAQWLNLQHLTIGAQ	240
DB	181	DEAVFCMLDMVMVEHYSKDGCATCTKLVRPKRHGTKSAEEELARAQWLNLQHLTIGAQ	240
OY	241	IGEFGFCAVLOGEYLGOKVAAYKNIKCDVTAQAFDEDTAVMTKMGEHLVRLGIYTLHQGL	300
DB	241	IGEFGFCAVLOGEYLGOKVAAYKNIKCDVTAQAFDEDTAVMTKMGEHLVRLGIYTLHQGL	300
OY	301	YIWEHVHSKGMNVNFLTFRGVALVNTAOQLFSLTIVAGMEYLESKKLVHNRDLARNILY	360
DB	301	YIWEHVHSKGMNVNFLTFRGVALVNTAOQLFSLTIVAGMEYLESKKLVHNRDLARNILY	360
OY	361	SEDIYIAKSDGLKAERKGDSSRLPVKWTAPAELAKHGKTFSKSDVNSFGVLLWEVESY	420
DB	361	SEDIYIAKSDGLKAERKGDSSRLPVKWTAPAELAKHGKTFSKSDVNSFGVLLWEVESY	420
OY	421	GRAYIPKMSLKEVSEAAVEKGYRMPEBECGPVNYHLMSCNEAEFARRPPFPFKLAETLAR	480
DB	421	GRAYIPKMSLKEVSEAAVEKGYRMPEBECGPVNYHLMSCNEAEFARRPPFPFKLAETLAR	480

QY 481 ELRSAGAPASVSGODADGSPRSQEP 507
 DB 481 ELRSAGAPASVSGODADGSPRSQEP 507

RESULT 2
 MATK_MOUSE STANDARD: . PRT; 505 AA.

AC P41242: 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112)
 DE (Tyrosine-protein kinase CTK) (Protein kinase NTK).
 GN MATK OR CTK OR NTK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 41-505 FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=94195789; PubMed=751815;
 RA Klages S., Adam D., Class K., Fargnoli J., Bolen J.B.,
 RA Penhallow R.C.;
 RT "Ctk: a protein-tyrosine kinase related to Csk that defines an enzyme
 family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:2597-2601(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Thymus;
 RX MEDLINE=94255451; PubMed=8197166;
 RA Chow L.M.L., Jarvis C.D., Hu Q., Nye S.H., Gervais F.G.,
 RA Velliste A., Mattis L.A.;
 RT "Ntk: a Csk-related protein-tyrosine kinase expressed in brain and T
 lymphocytes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4975-4979(1994).
 RN [3]
 RP SEQUENCE OF 41-505 FROM N.A.
 RC STRAIN=DDY/STD;
 RX MEDLINE=95206787; PubMed=7898936;
 RA Kaneko Y., Nonoguchi K., Fukuyama H., Takano S., Higashitsuji H.,
 RA Nishiyama H., Takenawa Y., Nakayama H., Fujita J.;
 RT "Presence of alternative 5' untranslated sequences and identification
 of cells expressing ctk transcripts in the brain and testis.";
 RL Oncogene 10:945-952(1995).
 CC -1- FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION
 OF HEMATOPOIETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF
 SRC-FAMILY MEMBERS IN BRAIN BY SPECIFICALLY PHOSPHORYLATING THEIR
 C-TERMINAL REGULATORY TYROSINE RESIDUE WHICH ACTS AS A NEGATIVE
 REGULATORY SITE. IT MAY PLAY AN INHIBITORY ROLE IN THE CONTROL OF
 T-CELL PROLIFERATION.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
 tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named Isoforms-2;
 CC Name-1:
 CC IsoId=P41242-1; Sequence=Displayed;
 CC Name-2:
 CC IsoId=P41242-2; Sequence=VSP_004966;
 CC Note=Minor isoform;
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, AND TO A LESSER EXTENT
 IN THE SPLEEN, THE THYMUS AND THE LIVER. ALSO FOUND IN THE T-CELL
 LINEAGE.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
 SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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CC -----
 CC EMBL: U05210; AAA18829.1; -
 CC EMBL: L27738; AAB59677.1; -
 CC EMBL: D45243; BAA08199.1; -
 CC PIR: I48926; I48926.
 CC PIR: I48926; I59296.
 CC HSSP: P11362; IFGK.
 CC MGD: MGI:99259; Matk.
 CC InterPro: IPR000719; Prot_Kinase.
 CC InterPro: IPR000980; SH2.
 CC InterPro: IPR001452; SH3.
 CC InterPro: IPR001452; SH3.
 CC InterPro: IPR001245; Tyr_kinase.
 CC Pfam: PF000017; SH2; 1.
 CC Pfam: PF000017; PKinase; 1.
 CC Pfam: PF00018; SH3; 1.
 CC PRINTS: PR00401; SH2DOMAIN.
 CC PRINTS: PR00109; TYRKINASE.
 CC ProDom: PD000001; Prot_Kinase; 1.
 CC ProDom: PD000093; SH2; 1.
 CC SMART: SM00252; SH2; 1.
 CC SMART: SM00326; SH3; 1.
 CC SMART: SM00219; Tyrc; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE: PS50002; SH3; 1.
 CC Transferrase: Tyrosine-protein kinase: ATP-binding; SH2 domain;
 CC SH3 domain; Phosphorylation; Alternative splicing.
 CC DOMAIN 61 108 SH3.
 CC FT DOMAIN 120 209 SH2.
 CC FT NP_BIND 233 481 PROTEIN KINASE.
 CC FT BINDING 239 247 ATP (BY SIMILARITY).
 CC FT ACT_SITE 260 260 ATP (BY SIMILARITY).
 CC FT VANSPLIC 350 350 BY SIMILARITY.
 CC FT T->TQ (in isoform 2).
 CC FT CONFLICT 43 43 /FTID=VSP_004966.
 CC FT SEQUENCE 105 106 HG -> QR (IN REF. 2).
 CC SQ SEQUENCE 505 AA; 56056 MW; 0A161C1FBFD6A53 CRC64;

Query Match 87.3%; Score 2332; DB 1; Length 505;
 Best Local Similarity 87.2%; Pred. No. 5; 1e-154;
 Matches 442; Conservative 26; Mismatches 37; Indels 2; Gaps 2;

QY 1 MAGRSLYSWRAFHGCDSEELPRVSPFLRAMHPPTPRMAGPTQCITKCEHT 60
 DB 1 MARSRKSVSWLAFEGMES-RDLPRVSPFLFGAMHPAPAAAKPT-RMAPGTQCKTCENS 58

QY 61 RPKPEELAFRRGDVVTILEACENKSWYVKKHHTSGQEGILAAAGALREDAISADPKLSLM 120
 DB 59 RPKPEELAFRRGDVVTILEACEDKSWYRAKHNGSGOGLLAAALRHGEALSTDPKLSLM 118

QY 121 PWFHCKISGOEAVQOOLPEDEGLFVRSARHPGQYVLCVSGRGVHYRYVLRHGHLLT 180
 DB 119 PWFHCKISGOEAVQOOLPEDEGLFVRSARHPGQYVLCVSGRGVHYRYVLRHGHLLT 178

QY 181 DEAVFFCMIMVMEHYSKDKGALCTKLVPRPKRHGTSKSAEELARAGMLNLQHLTLGAQ 240
 DB 179 DEAVFCFLMIMVMEHYTKDKGALCTKLVPRPKRHGTSKSAEELARAGMLNLQHLTLGAQ 238

QY 241 IGEGEFGAVLOGEYIGQVAVANKIKCDVTAQAFLEDETVAMTKMOHENTVRLGLVILHGL 300
 DB 239 IGEGEFGAVLOGEYIGQVAVANKIKCDVTAQAFLEDETVAMTKLOHRLVRLGLVILHGL 298

QY 301 YIVMEHYSKGNLVNLTFRGALVNTAQLOLPSLVAGSMYLSKTKLVHDLAARNLTV 360
 DB 299 YIVMEHYSKGNLVNLTFRGALVNTAQLOLPSLVAGSMYLSKTKLVHDLAARNLTV 358

QY 361 SEDIVAKVSDGLAKAEKRGDSSRLPVKWTAPALAKHGKFTSKSDVMSFGVLLMEVPSY 420

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Db 359 SEDLVAKVSDPGLAKERKLDSSRLPVKWTAEALKNGFTSSKSDVMSGVLMVEFSY 418
QY 421 GRAPYRMSLKEVSEAVEKGYRMEPEPCGPGPHVILMSQWEAPARRPFRLAEKLAR 480
Db 419 GRAPYRMSLKEVSEAVEKGYRMEPEPCGPGSVHTLMGSCWEAPARRPFRLAEKLGR 478
QY 481 ELRSAGAPASVSGQADGTSPPSQEP 507
Db 479 ELRSVGSAPAGQEAEGSAPTRSDP 505

RESULT 3
MATK_RAT
ID MATK_RAT STANDARD; PRT; 467 AA.
AC P41243;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112)
DE (Tyrosine-protein kinase CTK) (Protein kinase BAKK).
GN MATK OR CTK OR BAKK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-Sprague-Dawley; TISSUE=Hippocampus;
RX MEDLINE=95106341; PubMed=7807586;
RA Kuo S.S., Moran P., Gripp J., Armanini M., Phillips H.S., Goddard A.,
RA Caras I.W.;
RT Identification and characterization of Bakt, a predominantly brain-
RT specific non-receptor protein tyrosine kinase related to CSK.;
RL J. Neurosci. Res. 38:705-715(1994).
CC -1- FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION
CC OF HEMATOPOIETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF
CC SRC-FAMILY MEMBERS IN BRAIN.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- TISSUE SPECIFICITY: ENRICHED IN LYMPHOID TISSUES.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC -----
DR EMBL_L34542; AAA64524.1; -
DR PIR; I56579; I56579.
DR HSSP; P11362; IFGK.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_Kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

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DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW transferase; Tyrosine-protein kinase; ATP-binding; SH2 domain;
KW SH3 domain; phosphorylation.
FT DOMAIN 22 69
FT DOMAIN 81 170 SH2.
FT DOMAIN 194 443 SH2.
FT NP_BIND 200 208 ATP (BY SIMILARITY).
FT BINDING 221 221 ATP (BY SIMILARITY).
FT ACT_SITE 311 311 BY SIMILARITY.
SQ SEQUENCE 467 AA; 51896 MW; 283FE9348BB5FA8F CRC64;

Query Match 83.2%; Score 2221.5; DB 1; Length 467;
Best Local Similarity 89.3%; Pred. No. 2e-146;
Matches 417; Conservative 27; Mismatches 22; Indels 1; Gaps 1;

QY 42 MPTRRAPGTQCITCKCEHTRPKPELAFKRGDVYTLLEACENKSWYRVNHTSGQGLLA 101
Db 1 MPTQRAWAPGTQCWTCKCENSRRPKPELAFKRGDVYTLLEACEDKSWYRAKHSSGQGLLA 60
QY 102 AGALRERREALSDPKSLMPHFHGKISGQAVQQLPPEDGLFLVESARHPEDYLCVS 161
Db 61 AALRORREALSTDPKSLMPHFHGKISGQEAIDQLPPEDGLFLVESARHPEDYLCVS 120
QY 162 FGRDVHYRYLRHBDGLTIDEAVFCNLDMDVHYSKDGAICTKLVRRKRGKTSABE 221
Db 121 FGRDVHYRYLRHBDGLTIDEAVFCNLDMDVHYTRDGAICTKLVRRKRGKSAABE 180
QY 222 ELARAGMLNLQHLTLGAQIGEGEFGAVLQGEYLQKVAVNKIKCDVTQAFLDETAVM 281
Db 181 ELAKAGMLDLQHLTLGAQIGEGEFGAVLQGEYLQKVAVNKIKCDVTQAFLDETAVM 240
QY 282 KMGHENLVRLGLTYLHQGLYIWEHNSKGLNVLFTRGALVNTQQLQPSLHVAEGHE 341
Db 241 KLGHRNLVRLGLTYLHQGLYIWEHNSKGLNVLFTRGALVNTQQLQFALHVAEGHE 300
QY 342 YLESKRLVHRDLAARNILVSEDLVAVKVSDFGLAKAE-RKGLDSSRLPVKWTAEALKRGK 400
Db 301 YLESKRLVHRDLAARNILVSEDLVAVKVSDFGLAKAEALKRGKGLDSSRLPVKWTAEALKRGK 360
QY 401 FTSKSPVMSFGVILMEVFSTYGRAPYRMSLKEVSEAVEKGYRMEPEPCGPGPHVILMSSC 460
Db 361 FTSKSPVMSFGVILMEVFSTYGRAPYRMSLKEVSEAVEKGYRMEPEPCGPGPHVILMSSC 420
QY 461 WEAPARRPFRLAEKLARELSAGAPASVSGQADGTSPPSQEP 507
Db 421 WEAPARRPFRLAEKLARELSAGAPASVSGQADGTSPPSQEP 467

RESULT 4
CSK_CHICK
ID CSK_CHICK STANDARD; PRT; 450 AA.
AC P41239;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-Src kinase).
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92196083; PubMed=1372437;
RX Sabe H., Knudsen B., Okada M., Nada S., Nakagawa H., Hanafusa H.;
RT "Molecular cloning and expression of chicken C-terminal Src kinase:
RT lack of stable association with c-Src protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2190-2194(1992).

```

CC -1- FUNCTION: SPECIFICALLY PHOSPHORYLATES A TYROSINE ON THE SRC
 CC KINASE. THIS TYROSINE ACTS AS A NEGATIVE REGULATORY SITE.
 CC CAN ALSO ACT ON THE LYN AND FYN KINASES.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M85039; AAA51436.1; -;
 DR PIR; A41973; A41973.
 DR HSSP; P41240; ICSK.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00326; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; SH2 domain;
 DR SH3 domain; Phosphorylation.
 FT DOMAIN 9 70
 FT DOMAIN 82 171 SH2.
 FT DOMAIN 195 450 SH3.
 FT NP_BIND 201 209 PROTEIN KINASE.
 FT BINDING 222 222 ATP (BY SIMILARITY).
 FT ACT_SITE 314 314 BY SIMILARITY.
 FT MOD_RES 416 416 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 450 AA; 50751 MW; 5AA3C406AA4F246F CRC64;
 Query Match 46.9%; Score 1253.5; DB 1; Length 450;
 Best Local Similarity 53.9%; Pred. No. 1.6e-79;
 Matches 234; Conservative 84; Mismatches 113; Indels 3; Gaps 2;
 Oy 47 WAPETOCITCENTRPRKPGELAFRRKGVTVTLACENKSWYRVKHNHSGEGILLAGALR 106
 Db 8 WPSSTECIAKYNFNGHTAEODLPFSKGDVLTAVTKDPNKKAKNVY-GREGILPANYVQ 66
 Oy 107 ERELSADPKLSTLMPHFGKTSISGEOAVOQLPPEDGLFVRESARHGVDVLCVSPFGDV 166
 Db 67 KRESVKAGIKLSTLMPHFGKTSISGEOAVOQLPPEDGLFVRESARHGVDVLCVSPFGDV 126
 Oy 167 IHVFLARDGHLTIDEAVFPCNLDMVDEHYSKDGACCTKLVRKRKHGTSAGEELARA 226
 Db 127 EHYIIISSTKSLTIDEVYFENLMQVLEHTTDDGLCSRLIKRKVMEGYIAQADEFSRS 186
 Oy 227 GWLNLQHLTGLAIOIGEGFCAVLOGEYLQKVAVKIKCDVTAQAFLDETAVMTKQHE 286
 Db 187 GWALNMDKLKLLQIIGEGFCAVLOGEYLQKVAVKIKCDVTAQAFLDETAVMTKQHE 246

Oy 287 NLVRLGLYLHO--GLTYVMEVSKGNLVNPLRTGRALVNTAQLLOPSLHVAEGMYLE 344
 Db 247 NLVOLLGIVYEKSGGLIYVETYMAGKSLVDLRSRGSVGLGDCILKSLVCAAMEYLE 306
 Oy 345 SKRLVHDLARNLIVSEDLVAKVSDGLAKERRGLDSSRLPVKWTAPALKHGKFTSK 404
 Db 307 ANNFVHRDLAARNLVSEDLNIAKVSDFGLTKEASTQDTGKLPVKWTAPEALREKFFSTK 366
 Oy 405 SDVMSFGLLMEVSYGRAPPKMSLKEVSAVKEGTRMEPECCPGFVHYLMSSCEAE 464
 Db 367 SDVMSFGLLMEVSYGRAPPKMSLKEVSAVKEGTRMEPECCPGFVHYLMSSCEAE 426
 Oy 465 PARPPPKLAERL 478
 Db 427 PGRHPSFQRLREQL 440
 RESULT 5
 CSK_HUMAN
 ID CSK_HUMAN STANDARD; PRT: 450 AA.
 AC P41240.
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase) (Protein-
 DE tyrosine kinase CYL).
 GN CSK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93241739; PubMed-7683131;
 RA Breuninger A., Karn T., Strehardt K., Ruebsamen-Waigmann H.;
 RT "Characterization of the human CSK locus.";
 RL Oncogene 8:1365-1369(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92050797; PubMed-1945408;
 RA Partanen J., Armstrong E., Bergman M., Maekelae T.P., Hirvonen H.,
 RA Huebner K., Allitalo K.;
 RT "CYL encodes a putative cytoplasmic tyrosine kinase lacking the
 RT conserved tyrosine autophosphorylation site (Y416src).";
 RL Oncogene 6:2013-2018(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE-LUNG;
 RC MEDLINE-92073297; PubMed-1720539;
 RA Breuninger A., Holtrich U., Strehardt K., Ruebsamen-Waigmann H.;
 RT "Two additional protein-tyrosine kinases expressed in human lung;
 RT fourth member of the fibroblast growth factor receptor family and an
 RT intracellular protein-tyrosine kinase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10411-10415(1991).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 1-71.
 RX MEDLINE-94185778; PubMed-7511113;
 RA Borchert T.V., Mathieu M., Zeelen J.P., Courtneidge S.A.,
 RA Wierenga R.K.;
 RT "The crystal structure of human CSKSH3: structural diversity near the
 RT RT-Src and n-Src loop.";
 RL FEBS Lett. 341:79-85(1994).
 CC -1- FUNCTION: SPECIFICALLY PHOSPHORYLATES A TYROSINE ON THE SRC
 CC KINASE. THIS TYROSINE ACTS AS A NEGATIVE REGULATORY SITE.
 CC CAN ALSO ACT ON THE LYN AND FYN KINASES.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.

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 CC -----
 DR EMBL: X74765; CAB58562.1; -
 DR EMBL: X60114; CAA43713.1; -
 DR EMBL: X59932; CAA42556.1; -
 DR PIR: JH0559; JH0559.
 DR PDB: 1GSK; 31-JUL-94.
 DR PDB: 1BYG; 14-OCT-99.
 DR Genew: HGNC:2444; CSK.
 DR MIM: 124095; -
 DR GO: GO:0008022; F:protein C-terminus binding activity; TAS.
 DR GO: GO:0004713; F:protein tyrosine kinase activity; TAS.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR GO: GO:0000074; P:regulation of cell cycle; TAS.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR01245; Tyr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR Transferrase: Tyrosine-protein kinase; ATP-binding; SH2 domain;
 KW SH3 domain; phosphorylation; 3D-structure.
 FT DOMAIN 9
 FT DOMAIN 82 171
 FT DOMAIN 195 449
 FT NP_BIND 201 209
 FT BINDING 222 222
 FT ACT_SITE 314 314
 FT MOD_RES 416 416
 FT STRAND 12 16
 FT STRAND 20 20
 FT STRAND 25 26
 FT STRAND 27 27
 FT STRAND 30 30
 FT STRAND 32 33
 FT STRAND 35 41
 FT STRAND 45 46
 FT STRAND 51 51
 FT STRAND 53 54
 FT STRAND 57 61
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 FT STRAND 65 66
 SQ SEQUENCE 450 AA; 50704 MW; 431023A88C54E00C CRC64;
 Query Match 46.68; Score 1245.5; DB 1; Length 450;
 Best Local Similarity 54.18; Pred. No. 5.9e-79;
 Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;
 QY 47 MAFGTCITKCEHTPRKPEGLARPGDVVTILAECEKRSYRVKHNHTSGOEGLLAGALR 106
 DB 8 WPSGTETIAKYNHGTAEQDLPRCKGDLVLTIVAVTKDPNMYKAKNKY-GREGIIPANYVQ 66

QY 107 EREALSADPKLSIMPWFHGKISGQEAVALQPPEDGLFVRESARHFGDYVLCVSGRDY 166
 DB 67 KRGVAGACTGSLMPWFHGKISGQEAVALQPPEDGLFVRESARHFGDYVLCVSGRDY 126
 QY 167 IHRVLHRDGLTIDEAVFCNLMDEVYH SKDKAICTKLVPRKRHGTSAEDELAR 226
 DB 127 EHRVIMWASKLSIDEVEYFENLMJVEHTSDADGICFTRILPKWEGTVAADQEFYRS 186
 QY 227 GWLNLQHLFLGADIGGEGFAGVLOGEYLGOKAIVNKKDQVNAOFLDETAVMTKMOE 286
 DB 187 GVALNMKEKLTOTIGGEGDVALGDKRKNKVAKCIKNDATQAQFLABASVMTQURHS 246
 QY 287 NLVRLGLVLIHQ--GLYIVMEHVS KGNLVNFTTRGRALVNTAQLQFSLHVEGMEYLE 344
 DB 247 NLVQGLGVYIEERGGYIVTEYMAKSLVDYLRSGRVSIGDCLLFSLDVCENMEYLE 306
 QY 345 SKRLVHRDLAARNLVSEDLVAAYSDPGLAKARGLDSRLVYKVTAPALKHGFTSK 404
 DB 307 GNNFVHRDLAARNLVSEDLVAAYSDPGLAKARGLDSRLVYKVTAPALKHGFTSK 366
 QY 405 SDVMSFGVLLMEYFSGRAPHYPMKSLKEVSEAVEKGYRMPPEGCGDPYHVLMSQWEAE 464
 DB 367 SDVMSFGVLLMEYFSGRAPHYPMKSLKEVSEAVEKGYRMPPEGCGDPYHVLMSQWEAE 426
 QY 465 PARPPERKLAERL 478
 DB 427 AAMRPSFLQLREQL 440
 RESULT 6
 ID CSK_RAT STANDARD; PRT; 450 AA.
 AC P32577;
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase).
 GN CSK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=91226538; PubMed=1709258;
 RA Noda S., Okada M., McAnuley A., Cooper J.A., Nakagawa H.;
 RT "Cloning of a complementary DNA for a protein-tyrosine kinase that
 RT specifically phosphorylates a negative regulatory site of p60c-src."
 RT Nature 351:69-72(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=92105072; PubMed=1722201;
 RA Okada M., Noda S., Yamashita Y., Yamamoto T., Nakagawa H.;
 RT "CSK: a protein-tyrosine kinase involved in regulation of src family
 RT kinases."
 RT J. Biol. Chem. 266:24249-24252(1991).
 RL -1- FUNCTION: SPECIFICALLY PHOSPHORYLATES A TYROSINE ON THE SRC
 CC KINASE. THIS TYROSINE ACTS AS A NEGATIVE REGULATORY SITE.
 CC CAN ALSO ACT ON THE LYN AND FYN KINASES.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- TISSUE SPECIFICITY: ENRICHED IN LYMPHOID TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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CC EMBL: X58631; CAA41484.1; -
 DR PIR: S15094; S15094.
 DR PDB: 1K9A; 01-MAY-02.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00326; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TYRKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR Transferrase: Tyrosine-protein kinase: ATP-binding; SH2 domain;
 KW SH3 domain; Phosphorylation; 3D-structure.
 FT DOMAIN 9 70
 FT DOMAIN 82 171
 FT DOMAIN 195 445
 FT NP_BIND 201 209
 FT BINDING 222 222
 FT ACT_SITE 314 314
 FT MOD_RES 416 416
 FT SEQUENCE 450 AA; 50746 MW; 393DC8D737DAC67A CRC64;
 Query Match 46.5%; Score 1242.5; DB 1; Length 450;
 Best Local Similarity 54.1%; Pred. No. 9,4e-79;
 Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

QY 47 WAPGTCITRCENTPRPGLAERKGDVVTILECENKSWYRVKHNHSGEGLLAAGLR 106
 DB 8 WPGTECIARKNFNGHTAEODLPFCRGDVLITVAVTKDPNMYKAKNKV-GREGIIPANVY 66
 QY 107 EREHLSADPRLSLMPWPHGKISGGEAVOQLPPEDGLFVRESARHGEDVYLCVSGRDY 166
 DB 67 KREGVKAQTKLSLMPWPHGKITRQARLLYPPETGLFVRESSTNYPGDYTLCVSCGKV 126
 QY 167 IHYVLRDGHITFDEAVFCNLDVNEHYSKDKAGICTKLVRRKRGHGTSADEELARA 226
 DB 127 EHYRIMHASKLSIDEVEYFENLMQVLEHTTDDAGICTRLIKRVKVEGYAODEYRRS 186
 QY 227 GMLNLQHLTGAQIGGEFAGVLOGEYLGOKYAVNKKICDVTAAQLDETAVMTKQHE 286
 DB 187 GMLNLMKELKLTIGTIGGERGDVMTLGDYRGKNAVKCIKNDATAQAFLEASVNTQLRHS 246
 QY 287 NLVALLGVILHQ--GLTYVMEHVSQKLVNLFRTRGALVNTADLLOPSLHVAAGMEYLE 344
 DB 247 NLVOLLGVIVEEKGGLTYVEYMAKGLVYLRSGHVSGLGDCLLFESLDVCAMLEYLE 306
 QY 345 SKKLVHRDLAARNILVSEDIYAKVSDFGLAKEKGLDSSRLPYKWTAPALKIGKFTSK 404
 DB 307 GNNRVHHDLAARNVLYSEDNVAKSDGLIKREASTDTDTGLPKWTAPALIRKKTSTK 366
 QY 405 SDVWSFGVLLMEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPECCPGPVHVMSSCWEAE 464
 DB 367 SDVWSFGVLLMEVFSYGRAPYPRIPKDVVPRVEKGYKMDAPDCPPAVYDVMAKNCWILD 426
 QY 465 PARPPPRKLAELK 478
 DB 427 AATRPFLQLEKOL 440

RESULT 7

CSK_MOUSE
 ID CSK_MOUSE STANDARD; PRT: 450 AA.
 AC P41241; 003143;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase) (Protein-tyrosine kinase MPR-2).
 GN CSK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94195789; PubMed=7511815;
 RA Klages S., Adam D., Class K., Fargnoli J., Bolen J.B., Penhallow R.C.;
 RT "Csk: a protein-tyrosine kinase related to Csk that defines an enzyme family.";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:2597-2601(1994).
 RN [2]
 RP SEQUENCE OF 316-367 FROM N.A.
 RC SRAIN=C57BL/6; TISSUE=Embryonic brain;
 RX MEDLINE=9306484; PubMed=1281307;
 RA Giliardi-Hebenstreit P., Nieto M.A., Fraaij M., Mattei M.-G., Chestier A., Wilkinson D.G., Charney P.;
 RT "An Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain.";
 RL Oncogene 7:2499-2506(1992).
 CC -1- FUNCTION: SPECIFICALLY PHOSPHORYLATES A TYROSINE ON THE SRC KINASE. THIS TYROSINE ACTS AS A NEGATIVE REGULATORY SITE.
 CC CAN ALSO ACT ON THE LYN AND FYN KINASES.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- TISSUE SPECIFICITY: UNBIOGENOUS, BUT MOST ABUNDANT IN THYMUS AND SPLEEN, AS WELL AS IN NEONATAL BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
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RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Leukemic T-cell;
RX MEDLINE=96085119; PubMed=7495859;
RA Vogel L.B., Arthur R., Fujita D.J.;
RT "An aberrant lck mRNA in two human T-cell lines.";
RL Biochim. Biophys. Acta 1264:168-172(1995).
[6]
RN SEQUENCE FROM N.A.
RP TISSUE=Lymph;
RC MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pangue C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millar S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[7]
RN SEQUENCE OF 13-508 FROM N.A.
RP TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=20462621; PubMed=11009087;
RA Boncristiano M., Majolini M.B., D'Elia M.M., Pacini S., Valensin S.,
RA Olivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
RA Balderi C.T.;
RT "Defective recruitment and activation of ZAP-70 in common variable
RT immunodeficiency patients with T cell defects.";
RL Eur. J. Immunol. 30:2632-2638(2000).
[8]
RN SEQUENCE OF 367-508 FROM N.A.
RP MEDLINE=88217332; PubMed=2835736;
RX Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
RA "Expression of the lck tyrosine kinase gene in human colon carcinoma
RT and other non-lymphoid human tumor cell lines.";
RL Oncogene Res. 1:357-374(1987).
[9]
RN SEQUENCE OF 374-508 FROM N.A.
RP MEDLINE=87000726; PubMed=3489486;
RX Trevillian J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
RA Lima T.J.;
RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
RT p56lck.";
RL Biochim. Biophys. Acta 888:286-295(1986).
[10]
RN SEQUENCE OF 1-34 FROM N.A.
RP MEDLINE=89096891; PubMed=2850479;
RX Garvin A.M., Pawar S., March J.D., Perlmutter R.M.;
RA "Structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line.";
RL Mol. Cell. Biol. 8:3058-3064(1988).
[11]
RN SEQUENCE OF 1-34 FROM N.A.
RP MEDLINE=89313764; PubMed=2787474;
RX Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
RA Miyamoto N.G., Mak T.W.;
RT "Structure of the two promoters of the human lck gene: differential
RT accumulation of two classes of lck transcripts in T cells.";
RL Mol. Cell. Biol. 9:2173-2180(1989).
[12]
RN MASS SPECTROMETRY.
RP TISSUE=Breast cancer;
RX MEDLINE=21829512; PubMed=11840567;
RA Harris R.A., Yang A., Stein R.C., Lucy K., Brustein T., Herath A.,
RA Parekh R., Waterfield M.D., O'Hare M.D., Neville M.A., Page M.J.,
RA Zvelebil M.J.;
RT "Cluster analysis of an extensive human breast cancer cell line
RT protein expression map database.";
RL Proteomics 2:212-223(2002).
[13]
RN INTERACTION WITH PI3K.
RP MEDLINE=94067101; PubMed=7504174;
RX Vogel L.B., Fujita D.J.;
RA "The SH3 domain of p56lck is involved in binding to
RT phosphatidylinositol 3'-kinase from T lymphocytes.";
RL Mol. Cell. Biol. 13:7408-7417(1993).
[14]
RN INTERACTION WITH KHDRSL.
RP MEDLINE=95155308; PubMed=7852312;
RX Vogel L.B., Fujita D.J.;
RA "p70 phosphorylation and binding to p56lck is an early event in
RT interleukin-2-induced onset of cell cycle progression in
RT T-lymphocytes.";
RL J. Biol. Chem. 270:2506-2511(1995).
[15]
RN PHOSPHORYLATION OF TYR-504.
RP MEDLINE=92347326; PubMed=1639064;
RX Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
RA Amrein K.E., Autero M., Burn P., Alltalo K.;
RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
RT down regulates its catalytic activity.";
RL EMBO J. 11:2919-2924(1992).
[16]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 52-225.
RP MEDLINE=94203291; PubMed=7512222;
RX Eck M.J., Atweell S.K., Shoelson S.E., Harrison S.C.;
RA "Structure of the regulatory domains of the Src-family tyrosine
RT kinase Lck.";
RL Nature 368:764-769(1994).
[17]
RN X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 126-220.
RP MEDLINE=95173978; PubMed=7532720;
RX Mikol V., Baumann G., Keller T.H., Manning U.M., Zurini M.G.M.;
RA "The crystal structures of the SH2 domain of p56lck complexed with
RT two phosphopeptides suggest a gated peptide binding site.";
RL J. Mol. Biol. 246:344-355(1995).
[18]
RN X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS) OF 121-225.
RP MEDLINE=96177765; PubMed=8604142;
RX Tong L., Warren T.C., King J., Betageri R., Rose J., Jakes S.;
RA "Crystal structures of the human p56lck SH2 domain in complex with
RT two short phosphotyrosyl peptides at 1.0-A and 1.8-A resolution.";
RL J. Mol. Biol. 256:601-610(1996).
[19]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 118-225.
RP MEDLINE=98352059; PubMed=9685372;
RX Tong L., Warren T.C., Lukas S., Schembri-King J., Betageri R.,
RA Proudfoot J.R., Jakes S.;
RT "Carboxymethyl-phenylalanine as a replacement for phosphotyrosine in
RT SH2 domain binding.";
RL J. Biol. Chem. 273:20238-20242(1998).
[20]
RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 230-500.
RP MEDLINE=97100952; PubMed=8945479;
RX Yamaguchi H., Hendrickson W.A.;
RT "Structural basis for activation of human lymphocyte kinase Lck upon
RT tyrosine phosphorylation.";
RL Nature 384:484-489(1996).
[21]
RN -1- FUNCTIONAL: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Binds to phosphatidylinositol 3'-kinase (PI3K) from T
CC lymphocytes through its SH3 domain and to the tyrosine
CC phosphorylated form of KHDRSL/p70 through its SH2 domain.
CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER

[illegible]

ID	SRC	AVISS	STANDARD	PRT	568 AA.
236	TLGAQIGGGERAVLQGEYL	-QKAVKNIK	-CDVIAQAFLEDETA	AVMTKMOHNLVRLIG	293
268	RLEVKLVGGCGEGEVMWG	TGWTGTTT	RAIKTLKFGTMSPE	FLDAQYMKLRHKKLVOLA	327
294	VILHGLGILVMEHVS	KGNLVN	LRTGRALVNTAQL	LOESLHYAEGMEYLESKLVHRDL	353
328	VYSEEPITIVIEYMS	KSLDLDFL	KGEMGKLYLRLP	OLVDMAAQISMAVYERNNYHRDL	387
354	AARNITLVEDDLVAKV	SDGLAKA----	ERKGLDSSRLPYKWT	APALAKGKFTSKSDVMS	409
368	RAANITLVGENLVC	KVADFGLARL	IEDNEYTAROGAKFP	IKMTAPAEALALGGRFIKSDVMS	447
410	FGVILMEVFSYGR	AVYPKMSLKEVSP	AVKGRMEPECCPG	GVHYHLMSSCWEABARP	469
448	FGILLITLTTCGR	VPEYPCMGNGE	VLDRVERGRIMCP	PECPESLHDMSCMRDRBERP	507
470	PFKRLAEKL	478			
508	TFEYVLAQDL	516			
12	RESULT				
12	SRC_AVISS				
AC	PLA084:		STANDARD:	PRT:	568 AA.
DT	01-JAN-1990	(Rel. 13,	Created)		
DT	01-JAN-1990	(Rel. 13,	Last sequence update)		
DT	28-FEB-2003	(Rel. 41,	Last annotation update)		
DE	Tyrosine-protein	kinase	transforming protein SRC	(EC 2.7.1.112)	(P60-SRC).
GN	V-SRC.				
OS	Avian sarcoma virus	(strain S1).			
OX	Viruses; Retroid	viruses; Retroviridae;	Avian type C retroviruses.		
OX	NCBI_Taxid=11881;				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87064539;	PubMed=3097513;			
RA	Iikawa S., Hagino-Yamagishi K.,	Kawai S., Yamamoto T., Toyoshima K.;			
RT	"Activation of the cellular src	gene by transducing retrovirus."			
RL	Mol. Cell. Biol. 6:2420-2428	(1986).			
CC	-1- FUNCTION: THIS PHOSPHOPROTEIN,	REQUIRED FOR BOTH THE INITIATION			
CC	AND THE MAINTENANCE OF NEOPLASTIC	TRANSFORMATION, IS A PROTEIN			
CC	KINASE THAT CATALYZES THE	PHOSPHORYLATION OF TYROSINE RESIDUES			
CC	IN VITRO.				
CC	-1- CATALYTIC ACTIVITY: ATP + a	protein tyrosine = ADP + protein			
CC	tyrosine phosphate.				
CC	-1- SIMILARITY: BELONGS TO THE	TYR FAMILY OF PROTEIN KINASES. SRC			
CC	SUBFAMILY.				
CC	-1- SIMILARITY: Contains 1 SH2	domain.			
CC	-1- SIMILARITY: Contains 1 SH3	domain.			
DR	HSSP; P00523;	2Ptk.			
DR	InterPro: IPR000719;	Prot_kinase.			
DR	InterPro: IPR000980;	SH2.			
DR	InterPro: IPR001452;	SH3.			
DR	InterPro: IPR001245;	Tyr_pkinase.			
DR	Pfam; PF00017;	SH2; 1.			
DR	Pfam; PF00018;	SH3; 1.			
DR	PRINTS; PR00401;	SH2DOMAIN.			
DR	PRINTS; PR00452;	SH3DOMAIN.			
DR	PRINTS; PR00101;	TYRKINASE.			
DR	ProDom; PD000001;	Prot_kinase; 1.			
DR	ProDom; PD000093;	SH2; 1.			
DR	ProDom; PD000066;	SH3; 1.			
DR	SMART; SM00252;	SH2; 1.			
DR	SMART; SM00326;	SH3; 1.			
DR	SMART; SM00219;	TYRK; 1.			
DR	PROSITE; PS00107;	PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS00109;	PROTEIN_KINASE_TYR; 1.			
DR	PROSITE; PS00011;	PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00001;	SH2; 1.			
DR	PROSITE; PS00002;	SH3; 1.			

Tyrosine-protein kinase; Oncogene; Transferase; Phosphorylation;
 KW ATP-binding; Myristate; SH3 domain.
 FT LIPID 2 MYRISTATE.
 FT DOMAIN 81 142 SH3.
 FT DOMAIN 148 245 SH2.
 FT DOMAIN 267 520 PROTEIN KINASE.
 FT NP_BIND 273 281 ATP (BY SIMILARITY).
 FT BINDING 295 295 ATP (BY SIMILARITY).
 FT ACT_SITE 386 386 BY SIMILARITY.
 FT MOD_RES 416 416 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 568 AA: 63632 MW: 13777DB121F70998 CRC64;
 Query Match 27.5%; Score 734.5; DB 1; Length 568;
 Best Local Similarity 39.5%; Pred. No. 1.7e-43;
 Matches 168; Conservative 75; Mismatches 155; Indels 27; Gaps 10;
 QY 66 ELAFKRGDVYVTLLEACENKSWYRVKHHNSGQGLLAAGLRERALSADPKLSMPWFG 125
 DB 99 DLSFKKGERLQIVNNTEG-DMWLHSLTGTGTYPSNVAPSDSIQAE-----EWFYG 151
 QY 126 KISGOEAVQLOPPED--GLFLVRESARHPGDIYLCVS-----FGRDVIHYRLHRD-GH 177
 DB 152 KITRRESERLLNPNRPCTFLVRESEETTKGAYCLSDPDNARGLNVKHYIRKLDSG 211
 QY 178 LITDEAVFPCNLMDEYHYSKDKGAICTYL--VPRKRKGTSAEELARAGMLNLQHL 235
 DB 212 FYITSRTQPSLSQQLVAVYSKHAADGCHRLTNVCPTSKPQTGG---LAKDMEIPRESL 267
 QY 236 TLGAOIGEGFAGVLOGEYLG--OKYAVKNIK-CDVTAQAFIDETAVMTKMHEHNLRLIG 293
 DB 268 RLEVKLGQCCFGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAOVMKRLREKLYLA 327
 QY 294 VILHOGLYIVMHSVSKGNLVNFLRTGRALVNTAQLDPSLHVAEGMEYLSKKLYVRDL 353
 DB 328 VVSEEPYIVTEYMSKSLDLFLKGMKYLRLPOLVDAAQIASGMAYVERNNYVHRDL 387
 QY 354 AARNILVSEDLVAKYSDFGIARA-----ERKGLDSSRLPVKWTAPALAKGRTSKSDVMS 409
 DB 388 RAANILVGNLVCKYADDELALIDNETTAQAGAFPIKWTAPALAKGRTSKSDVMS 447
 QY 410 FGVLLMEVFSYGRAPPKMSLKEVSEAVEKGYRMEPECCPGPVHVLSSMCWEAPARP 469
 DB 448 FGIILLTELTTKGRVYPRGAVNREYLDQYRGIRMPCCPESLHLMQCRKDPDEEP 507
 QY 470 PERKL 474
 DB 508 TEYL 512
 RESULT 13
 SRC_AVIST STANDARD; PRT; 557 AA.
 AC P14085;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein SRC (BC 2.7.1.112) (P60-
 DE SRC).
 GN V-SRC.
 OS Avian sarcoma virus (strain S2).
 OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxID=11882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87064539; PubMed=3097513;
 RA Ikawa S., Hagino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.,
 RT "Activation of the cellular src gene by transducing retrovirus.";
 RL Mol. Cell. Biol. 6:2420-2428(1986).
 CC -FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION
 CC AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN
 CC KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
 CC IN VITRO.
 CC -CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein

tyrosine phosphate.
 CC -FUNCTION: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -SIMILARITY: Contains 1 SH2 domain.
 CC -SIMILARITY: Contains 1 SH3 domain.
 DR PIR: B25375; TVFVS2.
 DR HSSP: P00523; 2PTK.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_Kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Tyrosine-protein kinase; Oncogene; Transferase; Phosphorylation;
 KW ATP-binding; Myristate; SH3 domain; SH2 domain.
 FT LIPID 2 MYRISTATE.
 FT DOMAIN 81 142 SH3.
 FT DOMAIN 148 245 SH2.
 FT DOMAIN 267 520 PROTEIN KINASE.
 FT NP_BIND 273 281 ATP (BY SIMILARITY).
 FT BINDING 295 295 ATP (BY SIMILARITY).
 FT ACT_SITE 386 386 BY SIMILARITY.
 FT MOD_RES 416 416 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 557 AA: 62582 MW: B6C2A0CB99CEAFE CRC64;
 Query Match 27.5%; Score 734; DB 1; Length 557;
 Best Local Similarity 38.2%; Pred. No. 1.8e-43;
 Matches 175; Conservative 78; Mismatches 177; Indels 28; Gaps 11;
 QY 66 ELAFKRGDVYVTLLEACENKSWYRVKHHNSGQGLLAAGLRERALSADPKLSMPWFG 125
 DB 99 DLSFKKGERLQIVNNTEG-DMWLHSLTGTGTYPSNVAPSDSIQAE-----EWFYG 151
 QY 126 KISGOEAVQLOPPED--GLFLVRESARHPGDIYLCVS-----FGRDVIHYRLHRD-GH 177
 DB 152 KITRRESERLLNPNRPCTFLVRESEETTKGAYCLSDPDNARGLNVKHYIRKLDSG 211
 QY 178 LITDEAVFPCNLMDEYHYSKDKGAICTYL--VPRKRKGTSAEELARAGMLNLQHL 235
 DB 212 FYITSRTQPSLSQQLVAVYSKHAADGCHRLTNVCPTSKPQTGG---LAKDMEIPRESL 267
 QY 236 TLGAOIGEGFAGVLOGEYLG--OKYAVKNIK-CDVTAQAFIDETAVMTKMHEHNLRLIG 293
 DB 268 RLEVKLGQCCFGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAOVMKRLREKLYLA 327
 QY 294 VILHOGLYIVMHSVSKGNLVNFLRTGRALVNTAQLDPSLHVAEGMEYLSKKLYVRDL 353
 DB 328 VVSEEPYIVTEYMSKSLDLFLKGMKYLRLPOLVDAAQIASGMAYVERNNYVHRDL 387
 QY 354 AARNILVSEDLVAKYSDFGIARA-----ERKGLDSSRLPVKWTAPALAKGRTSKSDVMS 409
 DB 388 RAANILVGNLVCKYADDELALIDNETTAQAGAFPIKWTAPALAKGRTSKSDVMS 447
 QY 410 FGVLLMEVFSYGRAPPKMSLKEVSEAVEKGYRMEPECCPGPVHVLSSMCWEAPARP 469
 DB 448 FGIILLTELTTKGRVYPRGAVNREYLDQYRGIRMPCCPESLHLMQCRKDPDEEP 507
 QY 470 PERKLAELRLR-SAGAPASVSGDADGDSIPRSQE 506

DB 508 TFEYLAQFLIEDYLGILAMTPMEDKQEGPRGETASNKOE 545

RESULT 14

SRC_CHICK

ID SRC_CHICK STANDARD; PRT; 532 AA.

AC P00523; 090992; 091343; 091345; 092013; 098915;

DT 21-JUL-1986 (Rel. 01, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src) (c-Src).

GN SRC.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83155664; PubMed=6299580;

RA Takeya T., Hanafusa H.;

RT "Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus.";

RL Cell 32:881-890(1983).

RN [2]

RP REVISION TO 525.

RA Takeya T., Hanafusa H.;

RL Cell 34:319-319(1983).

RN [3]

RP SEQUENCE FROM N.A., AND PHOSPHORYLATION OF TYR-415 AND TYR-435.

RX MEDLINE=97008971; PubMed=8856081.

RA Wejland A., Neubauer G., Courtneidge S.A., Mann M., Wierenga R.K., Superti-Furga G.;

RT "The purification and characterization of the catalytic domain of Src expressed in Schizosaccharomyces pombe. Comparison of unphosphorylated and tyrosine phosphorylated species.";

RL Eur. J. Biochem. 240:756-764(1996).

RN [4]

RP SEQUENCE OF 1-18 AND 484-533 FROM N.A.

RX MEDLINE=91304409; PubMed=1712905;

RA Doral T., Levy J.B., Kang L., Brugge J.S., Wang L.H.;

RT "Analysis of CDNA's of the proto-oncogene c-src: heterogeneity in 5' exons and possible mechanism for the genesis of the 3' end of v-src.";

RL Mol. Cell. Biol. 11:4165-4176(1991).

RN [5]

RP ATP-BINDING SITE.

RX MEDLINE=84270751; PubMed=6431300;

RA Kamps M.P., Taylor S.S., Sefton B.M.;

RT "Direct evidence that oncogenic tyrosine kinases and cyclic AMP-dependent protein kinase have homologous ATP-binding sites.";

RL Nature 310:589-592(1984).

RN [6]

RP PHOSPHORYLATION.

RX MEDLINE=86028181; PubMed=2996780;

RA Gould K.L., Woodgett J.R., Cooper J.A., Buss J.E., Shalloway D., Hunter T.;

RT "Protein kinase C phosphorylates pp60src at a novel site.";

RL Cell 42:849-857(1985).

RN [7]

RP PHOSPHORYLATION OF TYR-415.

RX MEDLINE=82082387; PubMed=6273838;

RA Smart J.E., Oppermann H., Czernilofsky A.P., Purchio A.F., Erikson J.R., Bishop J.M.;

RT "Characterization of sites for tyrosine phosphorylation in the transforming protein of Rous sarcoma virus (pp60v-src) and its normal cellular homologue (pp60c-src).";

RL Proc. Natl. Acad. Sci. U.S.A. 78:6013-6017(1981).

RN [8]

RP PHOSPHORYLATION OF TYR-526.

RX MEDLINE=86151652; PubMed=2420005;

RA Cooper J.A., Gould K.L., Cartwright C.A., Hunter T.;

RT "Tyrosine 526 is phosphorylated in pp60c-src: implications for regulation.";

RL Science 231:1431-1434(1986).

RN [9]

RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.

RX MEDLINE=98070614; PubMed=9405157;

RA Williams J.C., Wejland A., Gonfalon S., Thompson A., Courtneidge S.A., Superti-Furga G., Wierenga R.K.;

RT "The 2.35 A crystal structure of the inactivated form of chicken Src: a dynamic molecule with multiple regulatory interactions.";

RL J. Mol. Biol. 274:757-775(1997).

RN [10]

RP STRUCTURE BY NMR OF 80-139.

RX MEDLINE=93279385; PubMed=8504863;

RA Yu H., Rosen M.K., Schneider S.L.;

RT "1H and 15N assignments and secondary structure of the Src SH3 domain.";

RL FEBS Lett. 324:87-92(1993).

RN [11]

RP STRUCTURE BY NMR OF 76-139.

RX MEDLINE=95063992; PubMed=7526465;

RA Feng S., Chen J.K., Yu H., Simon J.A., Schneider S.L.;

RT "Two binding orientations for peptides to the Src SH3 domain: development of a general model for SH3-ligand interactions.";

RL Science 266:1241-1247(1994).

CC -! FUNCTION: THE FUNCTION OF PP60-C-SRC IS UNKNOWN. IT IS EXPRESSED TO HIGH LEVELS, AND WITH A HIGH DEGREE OF KINASE ACTIVITY, IN CERTAIN FULLY DIFFERENTIATED CELLS SUCH AS NEURONS, PLATELETS AND MACROPHAGES.

CC -! CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.

CC -! ENZYME REGULATION: BECOMES ACTIVATED WHEN ITS MAJOR TYROSINE PHOSPHORYLATION SITE IS NOT PHOSPHORYLATED. IT CAN ALSO BE ACTIVATED BY POINT MUTATIONS AS WELL AS BY TRUNCATIONS AT THE C-TERMINAL END OR BY OTHER MUTATIONS.

CC -! PTM: Phosphorylated on Tyr-526 by c-Src kinase (CSK). The phosphorylated tail interacts with the SH2 domain thereby repressing kinase activity (by similarity).

CC -! MISCELLANEOUS: POLYOMA VIRUS MIDDLE T ANTIGEN FORMS A COMPLEX WITH PP60-C-SRC.

CC -! SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.

CC -! SIMILARITY: Contains 1 SH2 domain.

CC -! SIMILARITY: Contains 1 SH3 domain.

CC -----

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CC -----

DR EMBL; V00402; CAA23696.1; -

DR EMBL; J00844; AAA70194.1; -

DR EMBL; S43604; AAD13831.1; -

DR EMBL; S43616; AAD13835.1; -

DR EMBL; S43587; AAD13830.1; -

DR EMBL; S43609; AAD13832.1; -

DR EMBL; S43614; AAD13834.1; -

DR EMBL; S43579; AAB19353.2; -

DR PIR; A00630; TVCHS.

DR PDB; 1SRU; 31-MAY-94.

DR PDB; 1SRM; 31-MAY-94.

DR PDB; 2PTK; 24-DEC-97.

DR PDB; 1PRL; 07-FEB-95.

DR PDB; 1PRM; 07-FEB-95.

DR PDB; 1RLP; 07-FEB-95.

DR PDB; 1RLQ; 07-FEB-95.

DR PDB; 1NLO; 27-JAN-97.

DR PDB; 1NLP; 27-JAN-97.

DR PDB; 1F1W; 06-JUL-00.

DR PDB; 1F2F; 06-JUL-00.


```

DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; kinase.1.
DR Pfam: PF00017; SH2.1.
DR Pfam: PF00018; SH3.1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase.1.
DR ProDom: PD000093; SH2.1.
DR ProDom: PD000066; SH3.1.
DR SMART: SM00252; SH2.1.
DR SMART: SM00326; SH3.1.
DR SMART: SM00219; TYRKC.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00002; SH3.1.
DR Tyrosine-protein kinase; Proto-oncogene; Phosphorylation;
KW Transferrase; ATP-binding; Myristate; SH3 domain; SH2 domain;
KM 3D-structure.
FT INIT_MET 0 0
FT LIPID 1 1 MYRISTATE.
FT DOMAIN 80 141 SH3.
FT DOMAIN 147 244 SH2.
FT DOMAIN 266 519 PROTEIN_KINASE.
FT MOD_RES 11 11 PHOSPHORYLATION (BY PKC).
FT NP_BIND 272 280 ATP (BY SIMILARITY).
FT BINDING 294 294 ATP.
FT ACT_SITE 385 385 BY SIMILARITY.
FT MOD_RES 415 415 PHOSPHORYLATION (AUTO-).
FT MOD_RES 435 435 PHOSPHORYLATION (AUTO-).
FT MOD_RES 526 526 PHOSPHORYLATION (BY CSK).
FT CONFLICT 300 300 T -> N (IN REF. 1).
FT CONFLICT 500 500 K -> R (IN REF. 1).
FT STRAND 84 87 RN
FT STRAND 91 91 RP
FT STRAND 98 98 RA
FT STRAND 101 101 RT
FT TURN 103 104
FT STRAND 106 108
FT TURN 117 122
FT STRAND 123 125
FT TURN 128 132
FT STRAND 133 135
FT HELIX 136 138
FT TURN 139 140
FT TURN 142 144
FT TURN 146 147
FT STRAND 148 150
FT HELIX 154 161
FT TURN 162 162
FT TURN 168 169
FT STRAND 171 175
FT TURN 180 181
FT STRAND 183 188
FT STRAND 191 191

```

Query Match 27.4%; Score 733; DB 1; Length 532;
 Best Local Similarity 37.9%; Pred. No. 2e-43;
 Matches 173; Conservative 78; Mismatches 163; Indels 42; Gaps 11;

```

QY 66 ELAFRRGDVVTILEACENKSWYRKVHTSGOGLAAGALREKALSDPKLSLMPWFG 125
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 98 DISFKGERLQIVNNTG-DWMLASHLTGTGTGTPSNVAPSDSIQAE-----EWF 150
QY 126 KISGQAVVOLOPPED--GLFLVRESARHPGDVLCVS-----FGRDVIHYRLHRD-GH 177
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 151 KITRRESERLLNPNPGRGFLVRESEITTKGATCLSVSDPNAKGLNVAKHYKIRKLD 210

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```

QY 178 LTIDEAVFPCNLMDNVEHYSKDKGAICTKL--VRPKRHGKTSABEELARAGLNLQHL 235
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 211 FYTSRTQFSSLIQOLVAVYASKHADGICHLRTVNCPTSKPQTGG-----LAKDMEI 266
QY 236 TLGAQIGEEGFGAVLQGEVYLQ-KYAVKNIK-CDYTAQAFLEDTAVMTQMEHENVRLIG 293
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 267 RLEVKRGQGFGEVWVGWNGTTRVAKIKLKQKTSPEAFLEDAQVMKRLREKILQQLYA 326
QY 294 VILHOGILYVMEHVSNGNLVNFRLRTGRALVMTAQLDPSLVAEGMEYLSKTLVHRDL 353
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 327 VVSEEPITVLYTEMSGSLDPLFKGEMGYKLLPOLVDAAQIASGMAYVENMYVHRDL 386
QY 354 AARNILVSEDLVAKVSDGFLAKA---ERKGLDSSRLPYKWTAPALKHGKFTSKSDWS 409
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 387 RAANILVGNLVCKVADFGLARLIEDNEYTAQGAKEPIKMTAPEALATGREFTIKSDWS 446
QY 410 FCVLLMEVSYGRAPPKMSLKEVSAVAKGYRMEPECCPGPVHYLMSSGEAPARP 469
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 447 FGLLLELTGKGVPPGAVNREVLDPQVGRYRMPCEPCPSLHDMCKQWRKDPERR 506
QY 470 PERKLAELARELSAGAPASVSGDADSTSPRSQ 505
Db 507 TFEVLOAFI-----EDYFTSTEPQV 527.

```

RESULT 15
 SRC_AVISR STANDARD; PRT; 526 AA.
 AC P00525;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein SRC (BC 2.7.1.112) (P60-
 DE SRC).
 GN V-SRC.
 OS Avian sarcoma virus (strain RASV1441).
 OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.
 OX NCBI_Taxid=11894;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83059858; PubMed=6292477;
 RA Takeya T., Feldman R.A., Hanafusa H.;
 RT "DNA sequence of the viral and cellular src gene of chickens. 1.
 RT Complete nucleotide sequence of an EcoRI fragment of recovered avian
 RT sarcoma virus which codes for gp37 and pp60src.";
 RL J. Virol. 44:1-11(1982).
 RN [2]
 RP PHOSPHORYLATION OF TYR-416
 RX MEDLINE=81220979; PubMed=6264320;
 RA Neil J.C., Ghysdael J., Vogt P.K., Smart J.E.;
 RT "Homologous tyrosine phosphorylation sites in transformation-specific
 RT gene products of distinct avian sarcoma viruses.";
 RL Nature 291:675-677(1981).
 CC -1- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION
 CC AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN
 CC KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
 CC IN VITRO.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL: K00928; AAA42565.1; -

Job time : 19 secs

DR	PDB: 1OME: 08-MAR-96.	
DR	PDB: 1OME: 08-MAR-96.	
DR	InterPro: IPR000719; Prot_kinase.	
DR	InterPro: IPR00980; SH2.	
DR	InterPro: IPR01452; SH3.	
DR	InterPro: IPR01245; Tyr_kinase.	
DR	Pfam: PF00069; kinase; 1.	
DR	Pfam: PF00017; SH2; 1.	
DR	Pfam: PF00018; SH3; 1.	
DR	PRINTS: PR00401; SH2DOMAIN.	
DR	PRINTS: PR00452; SH3DOMAIN.	
DR	PRINTS: PR00109; TYRKINASE.	
DR	ProDom: PD000001; Prot_kinase; 1.	
DR	ProDom: PD00093; SH2; 1.	
DR	ProDom: PD000066; SH3; 1.	
DR	SMART: SM00252; SH2; 1.	
DR	SMART: SM00326; SH3; 1.	
DR	SMART: SM00219; TYRKc; 1.	
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.	
DR	PROSITE: PS50011; SH2; 1.	
DR	PROSITE: PS50002; SH3; 1.	
KW	Tyrosine-protein kinase; Oncogene; Transferase; Phosphorylation;	
KM	ATP-binding; Myristate; SH3 domain; SH2 domain; 3D-structure.	
FT	LIPID	2
FT	DOMAIN	81 142 SH3.
FT	DOMAIN	148 245 SH2.
FT	DOMAIN	267 517 PROTEIN_KINASE.
FT	NP_BIND	273 281 ATP (BY SIMILARITY).
FT	BLINDING	295 295 ATP (BY SIMILARITY).
FT	ACT_SITE	386 386 BY SIMILARITY.
FT	MOD_RES	416 416 PHOSPHORYLATION (AUTO-).
QC	SEQUENCE	526 AA; 58878 MW; 7DB3903FE0233EA9 CRC64;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2003, 09:48:37 ; Search time 44 Seconds

(without alignments)
2973.470 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671

Sequence: 1 MAGRSLVSWRAFHGDSAE.....PASVSGQDADGSTRSPSGEP 507

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_oranelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2544	95.2	523	4 Q9NST8	Q9NST8 homo sapien
2	2385.5	89.3	465	4 Q16176	Q16176 homo sapien
3	2277.5	85.3	511	11 Q64103	Q64103 mus sp. vnk
4	2214.5	82.9	465	11 Q9D6H7	Q9D6H7 mus musculu
5	2214.5	82.9	465	11 P70223	P70223 mus musculu
6	1243.5	46.6	450	11 Q8VCW1	Q8VCW1 mus musculu
7	1216.5	45.5	450	13 Q73786	Q73786 xenopus lae
8	1004.5	37.6	485	5 Q9Y1Z0	Q9Y1Z0 ephydalia f
9	979.5	36.7	723	5 Q9VCK8	Q9VCK8 drosophila f
10	976.5	36.6	467	5 Q77132	Q77132 hydra atten
11	751.5	28.1	509	11 Q91X65	Q91X65 mus musculu
12	742.5	27.8	526	15 Q93080	Q93080 rous sarcom
13	742	27.8	502	13 Q8GJ39	Q8GJ39 fugu rubrip
14	737.5	27.6	509	6 Q95M32	Q95M32 hylabates s
15	736	27.6	545	15 Q86362	Q86362 rous sarcom
16	735.5	27.5	509	6 Q95KR7	Q95KR7 salmrl scl

17	734.5	27.5	526	15 Q64994	Q64994 rous sarcom
18	733	27.4	546	15 Q86363	Q86363 rous sarcom
19	732.5	27.4	504	5 Q8WSU2	Q8WSU2 ephydalia f
20	730.5	27.3	526	15 Q07461	Q07461 rous sarcom
21	730.5	27.3	526	15 Q60567	Q60567 rous sarcom
22	730.5	27.3	526	15 Q64993	Q64993 rous sarcom
23	730	27.3	495	5 Q8WSU4	Q8WSU4 ephydalia f
24	730	27.3	523	15 Q85477	Q85477 rous sarcom
25	729	27.3	535	15 Q92957	Q92957 rous sarcom
26	728.5	27.3	535	15 Q64817	Q64817 avian sarco.
27	724	27.1	1620	5 Q9VW86	Q9VW86 drosophila
28	723.5	27.1	526	15 Q92806	Q92806 rous sarcom
29	716.5	26.8	502	13 Q9DDK6	Q9DDK6 salmo salar
30	715	26.8	542	11 Q9J10	Q9J10 rattus norv
31	711	26.6	488	13 Q13064	Q13064 xenopus lae
32	710	26.6	541	11 Q99PW1	Q99PW1 rattus norv
33	706	26.4	499	11 Q8K2M8	Q8K2M8 mus musculu
34	706	26.4	541	11 Q8CBP1	Q8CBP1 mus musculu
35	703	26.3	491	11 Q8CE10	Q8CE10 mus musculu
36	702	26.3	541	11 Q8C762	Q8C762 mus musculu
37	698	26.1	525	13 Q8AWF1	Q8AWF1 brachydantio
38	698	26.1	537	11 Q62844	Q62844 rattus norv
39	697	26.1	812	15 Q85466	Q85466 y73 sarcoma
40	697	26.1	823	6 Q9TTY2	Q9TTY2 canis famil
41	695	26.0	505	4 Q961N1	Q961N1 homo sapien
42	694	26.0	527	13 Q91952	Q91952 xiphophorus
43	693.5	26.0	470	5 Q8WSU3	Q8WSU3 ephydalia f
44	691.5	25.9	496	13 Q93411	Q93411 xenopus lae
45	689.5	25.8	527	5 Q9Y121	Q9Y121 ephydalia f

ALIGNMENTS

RESULT 1
ID Q9NST8 PRELIMINARY; PRT; 523 AA.
AC Q9NST8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKEZP434N1212.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Duesterhoeft A., Lauber J., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AL137754; CAB70906.1; -;
DR HSSP; P11362; 1FGK.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase.1.
DR Pfam; PF00017; SH2.1.
DR Pfam; PF00018; SH3.1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase.1.
DR ProDom; PD000093; SH2.1.
DR SMART; SM00325; SH2.1.
DR SMART; SM00326; SH3.1.
DR SMART; SM00219; Tyrc.1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM.1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR.1.
DR PROSITE; PSS0001; SH2.1.

DR PROSITE; PS50002; SH3; 1.
 KW Hypothetical protein; Kinase; SH3 domain; Transferase;
 FT Tyrosine-protein kinase.
 FT NON_TER
 SQ SEQUENCE 523 AA; 57776 MW; C246280FD7890AFE CRC64;

Query Match 95.2%; Score 2544; DB 4; Length 523;
 Best local similarity 96.4%; Pred. No. 3.7e-198;
 Matches 488; Conservative 1; Mismatches 5; Indels 12; Gaps 1;

QY 2 AGRGSLVSMRARRHGCOSAEELPRVSPRFLRAHPPVSRAPMRAPRPAQTCITCKEHR 61
 DB 30 AGRG-----SGAPRQVSPRFLRAHPPVSRAPMRAPRPAQTCITCKEHR 77
 QY 62 PRGELAFRRKGDVVTILEACENKSWYRVKHNHSGOGLLAAGALRREALSADPKSLMP 121
 DB 78 PRGELAFRRKGDVVTILEACENKSWYRVKHNHSGOGLLAAGALRREALSADPKSLMP 137
 QY 122 WPHGKISGOEAVQOOLPPEDGLFLVRESARHPGDVLYVSGRDVTHYVNLHRDGLTID 181
 DB 138 WPHGKISGOEAVQOOLPPEDGLFLVRESARHPGDVLYVSGRDVTHYVNLHRDGLTID 197
 QY 182 EAVFPCNLMDVNEHYSKDKGATCTKLYPRKRKHGTSABEELARAGWLNLOHTLGAQI 241
 DB 198 EAVFPCNLMDVNEHYSKDKGATCTKLYPRKRKHGTSABEELARAGWLNLOHTLGAQI 257
 QY 242 GGEFGAVLQGEYLGQKVAVKNKCDVTQAQFLDETAVMTKQHEMLVRLGLVILHOGY 301
 DB 258 GGEFGAVLQGEYLGQKVAVKNKCDVTQAQFLDETAVMTKQHEMLVRLGLVILHOGY 317
 QY 302 IYMEHVSCKNLVNFRTGRALVNTAQLQFSLHVAEGMEYLESKLVHRDLAARILVS 361
 DB 318 IYMEHVSCKNLVNFRTGRALVNTAQLQFSLHVAEGMEYLESKLVHRDLAARILVS 377
 QY 362 EDLVAVSPFGLAKKERKGLDSSRLPVKWTAPALKHGFTSKSDVMSGVLLMEVSYG 421
 DB 378 EDLVAVSPFGLAKKERKGLDSSRLPVKWTAPALKHGFTSKSDVMSGVLLMEVSYG 437
 QY 422 RAPPYPMSLKEVSEAVEKGRMEPPGCGPVHVLMSGCEAEAPARRPPFKLAELARE 481
 DB 438 RAPPYPMSLKEVSEAVEKGRMEPPGCGPVHVLMSGCEAEAPARRPPFKLAELARE 497
 QY 482 LRSAGAPASVSGDADGSTSPRSQEP 507
 DB 498 LRSAGAPASVSGDADGSTSPRSQEP 523

RESULT 2
 016176 PRELIMINARY; PRT; 465 AA.
 AC 016176;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE Lsk protein.
 GN LSK.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94268844; PubMed-7516063;
 RA McVicar D.W., Lal B.R., Lloyd A., Kawamura M., Chen Y.Q.; Zhang X.,
 RA Staples J.E., Ortaldo J.R., O'Shea J.J.;
 RT "Molecular cloning of lsk, a carboxyl-terminal src kinase (csk)
 RT related gene, expressed in leukocytes.";
 RT Oncogene 9:2037-2044(1994).
 CC -I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC EMBL; S71669; AAB30995.1; -;
 DR HSSP; P11362; IFGK.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00006; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TyrcK; 1.
 DR PROSITE; PS50019; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 465 AA; 51908 MW; 504B4E8078320C35 CRC64;

Query Match 89.3%; Score 2385.5; DB 4; Length 465;
 Best local similarity 98.1%; Pred. No. 2.4e-185;
 Matches 457; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 42 MPTRRAPGTCITCKEHRPRKPGELAFRRKGDVVTILEACENKSWYRVKHNHSGOGLLA 101
 DB 1 MPTRRAPGTCITCKEHRPRKPGELAFRRKGDVVTILEACENKSWYRVKHNHSGOGLLA 60
 QY 102 AGALRREALSADPKSLMPWFHKGKISGOEAVQOOLPPEDGLFLVRESARHPGDVLYCVS 161
 DB 61 AGALRREALSADPKSLMPWFHKGKISGOEAVQOOLPPEDGLFLVRESARHPGDVLYCVT 120
 QY 162 FGRDVIHYVNLHRDGLTIDEAVFPCNLMDVNEHYSKDKGATCTKLYPRKRKHGTSABE 221
 DB 121 FGRDVIHYVNLHRDGLTIDEAVFPCNLMDVNEHYSKDKGATCTKLYPRKRKHGTSABE 180
 QY 222 ELARAGWLNLOHTLGAQIGGEFGAVLQGEYLGQKVAVKNKCDVTQAQFLDETAVM 281
 DB 181 ELARAGWLNLOHTLGAQIGGEFGAVLQGEYLGQKVAVKNKCDVTQAQFLDETAVM 239
 QY 282 KMQHEMLVRLGLVILHOGYIYMEHVSCKNLVNFRTGRALVNTAQLQFSLHVAEGME 341
 DB 240 KMQHEMLVRLGLVILHOGYIYMEHVSCKNLVNFRTGRALVNTAQLQFSLHVAEGME 299
 QY 342 YLESKLVHRDLAARILVSEDLVAVSPFGLAKKERKGLDSSRLPVKWTAPALKHGFT 401
 DB 300 YLESKLVHRDLAARILVSEDLVAVSPFGLAKKERKGLDSSRLPVKWTAPALKHGFT 359
 QY 402 TSKSDVMSGVLLMEVSYGRAPYPMKSLKEVSEAVEKGRMEPPGCGPVHVLMSGCM 461
 DB 360 TSKSDVMSGVLLMEVSYGRAPYPMKSLKEVSEAVEKGRMEPPGCGPVHVLMSGCM 419
 QY 462 EAEPPARRPPFKLAELARELSAGAPASVSGDADGSTSPRSQEP 507
 DB 420 EAEPPARRPPFKLAELARELSAGAPASVSGDADGSTSPRSQEP 465

RESULT 3
 064103 PRELIMINARY; PRT; 511 AA.
 AC 064103;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE VNK protein.
 GN VNK.
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95178994; PubMed-7874011;
 RA Ershler M.A., Krivtsov A.V., Krotkova A.V., Bellavskil A.V.,
 RA Visser J.V.;
 RT "VNK--a new gene for nonreceptor protein-tyrosine kinase, expressed


```
OY      222 ELARBGWLLNLOHLNLGAOIGSEBEGVALOGELTQKVAKVNIKCOVTQAOFIDETAVMT 281
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      180 ELAKGGLMDLDLHLLLGAGIIGBEGBVALDGGELTGOKVAVKNIKCVOYTQAOFIDETAIVMT 239
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      282 KMÖHENVLRLGVIIHQGLIYMEHVSKGNLVNFTLRGRALVNTAOLLOFSLHVEGME 341
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      240 KLÖHNVLRLGVIIHQGLIYMEHSVKNONLVFLTRGRALVSTSQLLOFALHVEGME 299
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      342 YLESKKLVHRDLAAARNILVSEDLYAVKSOPGLAKARKGIDSSRLPVYKMTAPALAHGKF 401
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      300 YLESKKLVHRDLAAARNILVSEDLYAVKSPFGLAERKGIDSSRLPVYKMTAPALKNGRF 359
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      402 TSKSDVMSFGVLLMWEFYSYGRAPIPKMSLKEVSEAEKGYRMBPEGCPCPVHYLMSCW 461
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      360 SKSUDVMSFGVLLMWEFYSYGRAPIPKMSLKEVSEAEKGYRMPPDGCPCSVHTLMGSCW 419
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      462 EAEPARRPERKLIAELISAGAPASVSODCDADCSRPQEP 507
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      420 EAEPRRRPERKIVEIGRELNSVGSAAGGCEAGSGAPTRODP 465
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

RESULT 5
P70223
ID P70223
PRELIMINARY;
PRT; 465 AA.

DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE HYL tyrosine kinase.
GN MARK OR HYLTK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBA x C57Bl/6; TISSUE=Embryonic stem;
RX MEDLINE=96280730; PubMed=8694808;
RA Hamaguchi I., Yamaguchi N., Suda T., Iwama A., Hirac A., Hashiyama M.,
RA Alizawa S.T., Suda T.;
RT "Analysis of CSK homologous kinase (CHK/HYL) in hematopoiesis by
RT utilizing gene knockout mice".
RL Biochem. Biophys. Res. Commun. 224:177-179(1996).
CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL: X83972; CAA58806.1; -.
DR HSSP: P11362; IFGK.
DR MGD: MGI:99259; Matk.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF000069; pkinase; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
DR ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 465 AA; 51571 MW; 24c2DBA7f1a08A3e9 CRC64;

Query Match	82.98;	Score 2214.5;	DB 11;	Length 465;
Best Local Similarity	89.58;	Pred. No. 1.9e-171;		
Matches 417;	Conservative 24;	Mismatches 24;	Indels 1;	Gaps 1;

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OY      4Z MPRRRAPGQCITCKEHTRPKPGELAPKGOVYITLACENCSMYRXKHTHSGOELLA 100
Db      1 MPT-RRAPGQOCTTKCENSRPKPGELAFKGMVITLACBCKSMYRKHNGSGOELLA 59
OY      102 AGALREREALSDAPKJSLMPWFHGKISGGEAVOQLOQPEDELLFVRESARHPGDIYCVS 161
Db      60 AALRGEALSTDPKJSLMPWFHGKISGGEAIQLOQPEDELLFVRESARHPGDIYCVS 119
OY      162 FGRDVIHYRVLHNDGHLTIDEAVFCNLMNDWMEHXSCKGAKICRYLAPRKHHTKSAEE 221
Db      120 FGRDVIHYRVLHNDGHLTIDEAVFCNLMNDWMEHTKKGAKICRYLAPRKHHTKSAEE 179
OY      222 ELARAGWLMLQHLTLTGAQIGSGEFGAVLOGEYLCQKAAVANNIKCDYTAQAFIDETAVMT 281
Db      180 ELAKAGWLMLDQHLTLTGAQIGSGEFGAVLOGEYLCQKAAVANNIKCDYTAQAFIDETAVMT 239
OY      282 KMOHENLVRLGYILHQGLTYMEHVSCKNLVNFRTGRALVMTAQLLQSLVAAGME 341
Db      240 KLOHRLNVRLGYILHNGLYIWEHVSCKNLVNFRTGRALVMTSOLQFALVAAGME 299
OY      342 YLESKRLVHDLAARNILVSEDLVAKVSPFGAKERKGLDSSRLPYVMTAPALAKHGF 401
Db      300 YLESKRLVHDLAARNILVSEDLVAKVSPFGAKERKGLDSSRLPYVMTAPALAKHGF 358
OY      402 TSKDVMSEFVLLMEVFSYGRAPYPRKMSLKEVSEAVEKGYRMEPEGCGPQGVHVLMSCW 461
Db      360 TSKDVMSEFVLLMEVFSYGRAPYPRKMSLKEVSEAVEKGYRMEPEGCGPQGVHVLMSCW 419
OY      462 EADPARPPPRKLAETLARELSACAPASVSSQDDADGSTSPRSQEP 507
Db      420 EADPARPPPRKLAETLARELSVSGSPAGQDEHSSAPRPSQEP 465

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RESULT 6

ID	Q8BYCW1	PRELIMINARY:	PRT:	450 AA.
AC	Q8BYCW1			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, last annotation update)			
DE	C-src tyrosine kinase.			
GN	CSK.			
OS	Mus musculus (mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Colon;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.			
DR	EMBL: BC018394; AAH18394.1; .			
DR	MED: MGI:88537; CSK.			
DR	InterPro: IPR000719; Prot_kinase.			
DR	InterPro: IPR000980; SH2.			
DR	InterPro: IPR001452; SH3.			
DR	InterPro: IPR001245; Tyr_kinase.			
DR	Pfam: PF00069; pkinase; I.			
DR	Pfam: PF00017; SH2; 1.			
DR	Pfam: PF00018; SH3; 1.			
DR	PRINTS: PRO0401; SH2DOMAIN.			
DR	PRINTS: PRO0109; TYRKINASE.			
DR	ProDom: PD000001; Prot_kinase; 1.			
DR	ProDom: PD000093; SH2; 1.			
DR	ProDom: PD000066; SH3; 1.			
DR	SMART: SM00252; SH2; 1.			
DR	SMART: SM00326; SH3; 1.			
DR	SMART: SM00219; TYRKC; 1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE: PSS0109; PROTEIN_KINASE_TYR; 1.			

DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SO SEQUENCE 450 AA; 50716 MW; E8D3EC9357B86277 CRC64;

Query Match 46.6%; Score 1243.5; DB 11; Length 450;
 Best Local Similarity 54.1%; Pred. No. 1.5e-92;

Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

QY 47 WAPGTCITKCEHTPRPGELARFGDVVITILEACENKSWYRVKHHHTSGDEGLAAGLR 106
 DB 8 WPGTEBIAKYNFHGTAEDLPFCCKGDLTVAVTKDPNMYKAKNKV-GREGIIPANYQ 66
 QY 107 EREALSDPKLSLMPWFHKGKISGOEAVOOLPPEDGFLVRESARHPGDVLCVSPRDY 166
 DB 67 KREGVAKGKTLSTLMPWFHKGKIRQAEKRLLYPETGLFVRESINYPGDVTLVCSCGKY 126
 QY 167 IHVRLRGDLITIDEAVFPCNLMDVNEHYSKDKGALCTKLVPRKRGHTKSABEELARA 226
 DB 127 EHYRIMYHASKLSIDEVEYFENLMQLYEHYTTDADGLCTRLIKPKVEGTVAADDEFYRS 186
 QY 227 GWLNLQHLTGLGQIGEGEYVLOGEYLGOKYAVKIKCDVTAQAFLDATAVTKQHE 286
 DB 187 GWALNKKELKLTQIGEGEGDVALGDRGNKYAVKICKNDATAQAFIAEASVMTQLRHS 246
 QY 287 NLVRLGVLILH--GLYIVNEHYSKGLVNFRTGRALVNTAQLLOESLHVAEGMYLE 344
 DB 247 NLVQLLGVLIVEEKGGLITVEYMAKGLVDYLSRGRSVLGDCCLFSLDVCAMETYLE 306
 QY 345 SKRLVHRDLAARNILVSEDLVAKVSPGLAKAEKRGDSRLPYKWTAPALKHGFTSK 404
 DB 307 GNNFVRHDLAARNVIVSEDNVAKVSDGLKKAASSTQDFTGKLPKYWTAPALRKRFSTK 366
 QY 405 SDVWSFGLLMEYFSTGRADYPKMSLKEVSEAVEKGYRMEPPGCGPVAHVLMSSCEAE 464
 DB 367 SDVWSFGLLMEYFSTGRADYPKMSLKEVSEAVEKGYRMEPPGCGPVAHVLMSSCEAE 426
 QY 465 PARPPPRKLAELK 478
 DB 427 AATPTPLQLREOL 440

RESULT 7
 073786 PRELIMINARY; PRT; 450 AA.
 AC 073786;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE C-Src kinase.
 GN CSK.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_Taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Murphy S.M., Morgan D.O.;
 RT "Identification of Xenopus c-Src Kinase (CSK) using a genetic screen
 RT for suppressors of c-Src activity in the budding yeast, *Saccharomyces*
 RT *cerevisiae*.";
 RU Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; AF052430; AAC05835.1; -;
 DR HSSP; P41240; 1CSK.
 DR InterPro: IPR000719; ProL_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase.1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.

DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; ProL_kinase; 1.
 DR PRODOM; PD000093; SH2; 1.
 DR PRODOM; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SO SEQUENCE 450 AA; 50807 MW; F02FE0357679BA53 CRC64;

Query Match 45.5%; Score 1216.5; DB 13; Length 450;
 Best Local Similarity 52.7%; Pred. No. 2.4e-90;
 Matches 233; Conservative 83; Mismatches 119; Indels 7; Gaps 3;

QY 47 WAPGTCITKCEHTPRPGELARFGDVVITILEACENKSWYRVKHHHTSGDEGLAAGLR 106
 DB 8 WQAGIECIANYDFGKAEDLDGKGEVLTVAVTKDPNMYKAKNKV-GRVGFIPANYQ 66
 QY 107 EREALSDPKLSLMPWFHKGKISGOEAVOOLPPEDGFLVRESARHPGDVLCVSPRDY 166
 DB 67 KREGVAKGKTLSTLMPWFHKGKIRQAEKRLLYPETGLFVRESINYPGDVTLVCSCGKY 126
 QY 167 IHVRLRGDLITIDEAVFPCNLMDVNEHYSKDKGALCTKLVPRKRGHTKSABEELARA 226
 DB 127 EHYRIIYSSKGLSIDEVEYFENLMQLYEHYTTDADGLCTNLIRKRLMEGTVAADDEFYRS 186
 QY 227 GWLNLQHLTGLGQIGEGEYVLOGEYLGOKYAVKIKCDVTAQAFLDATAVTKQHE 286
 DB 187 GWALNKKELKLTQIGEGEGDVALGDRGNKYAVKICKNDATAQAFIAEAMVMTQLRHS 246
 QY 287 NLVRLGVLILH--OGLYIVNEHYSKGLVNFRTGRALVNTAQLLOESLHVAEGMYLE 344
 DB 247 NLVQLLGVLIVEEKGGLITVEYMAKGLVDYLSRGRSVLGDCCLFSLDVCAMETYLE 306
 QY 345 SKRLVHRDLAARNILVSEDLVAKVSPGLAKAEKRGDSRLPYKWTAPALKHGFTSK 404
 DB 307 SNNFVRHDLAARNVIVSEDNVAKVSDGLKKAASSTQDFTGKLPKYWTAPALRKRFSTK 366
 QY 405 SDVWSFGLLMEYFSTGRADYPKMSLKEVSEAVEKGYRMEPPGCGPVAHVLMSSCEAE 464
 DB 367 SDVWSFGLLMEYFSTGRADYPKMSLKEVSEAVEKGYRMEPPGCGPVAHVLMSSCEAE 426
 QY 465 PARPPPRKLAELK---AREL 482
 DB 427 PKQPTPLQLREOLHIAKEL 448

RESULT 8
 09Y120 PRELIMINARY; PRT; 485 AA.
 AC 09Y120;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Protein tyrosine kinase.
 GN EPTK11.
 OS Ephydatia fluviatilis.
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
 OC Haplosclerida; Spongillidae; Ephydatia.
 OX NCBI_Taxid=31330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99246375; Pubmed-10229566;
 RA Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
 RA Miyata T.;
 RT "Extensive gene duplication in the early evolution of animals before

Query Match	37.6%	Score 1004.5	DB 5	Length 485
Best Local Similarity	42.2%	Pred. No. 4.6e-73		
Best 199, Conservative	94	Mismatches 138	Indels 41	Gaps 8

QY	47	WAPGOSCTTCKENHPKRGELAFRRGGVUUTLEACENSKSVYKHNHSGOELLAAAGLR	106
Db	5	WAVGTETCIGKTNFPSSPHDLPRFKGDDLVIYAFSPKDPNMYKARE-DGLESMIPPNYQ	63
QY	107	E-----REALSDP-----KSLMFWFNKLTSGOEAPOOL	136
Db	64	EKVAVGASAPORPGRPVLSAPORVADNDAAMNHASKGAVOLKTTMPWFHGRISREDAEKL	123
QY	137	QRPEDGELTVEESANHPGDYULCVSFFGADVILHYRLNHD-GILTLIDEAFPCNDMYEH	195
Db	124	TPPKNRRFLVRESQNPEDYTLCVSYDGRVEVRYRRNREKGLVTVDDDEYFNNLTKLYEH	183
QY	196	YSKDKGALCTKLIVPRKRKHGTK---SABEELAFARAGMLNLOHLTVGAOIGEEGFAGVLOG	252
Db	184	YQKEADGCTFLKAPVYDEKGGHLPVVDVNDREKEMWLPKASLKLKSLGKEFEFEWMLG	243
QY	253	EYLCQKAAVK---NIKCDVTAQAFLEDAVYTKQKHENLYRLGVILLHQG-LYTVMEHY	307
Db	244	DYEEKRAMKSMKDHCLKDEKAKTOFELASVSTVTLRHNFNLVCLISDNDNYITLTEM	303
QY	308	SKGNLYNLPRTGRALVNTAOLLOESLVAEGMEYLESKIYHRDLAARNTLVSDIYAK	367
Db	304	AKGSLIDYLRSGRAVITKQONIDFARVYKGMVYLESQNFVHRDLAARNTLVAEENYAK	363
QY	368	VSDGELAKAERK-GIDSSRLPVKWTAPALPKHGXSTSDVSWFSFVILLMEVYSYGRAPY	426
Db	364	VSDGELAKSSSNVYQEGAKLFPYKWTAPALPKENKSNNTDVMWFSFVILLMEIYSYGRVYP	423
QY	427	KMSLKEVSEAVKGYRMRPBGCGPQVHYVLMSSCWEADPARPPRKLAEKL	478
Db	424	RVPEEDVANNHENGRYMESPGCGPQIYKIMMDCKEKDPGSPGPNTRLEKAL	475

RESULT	9
Q9VGR8	PRELIMINARY; PRT; 723 AA.
ID	Q9VGR8
AC	Q9VGR8; Q9VGR9;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DR	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE	Cg17309 protein.
CN	Cg17309.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Berkely;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Maniatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Balcer F.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Crowe C., Ferreira S., Fleischmann W.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA	Hosltin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
RA	Jaitani M., Kalush F., Kapran G.H., Ke Z., Kennison J.A., Kerchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Mishina N.V., Mobarry C., Morris S., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinett K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Stimpson M., Skupski M.P., Smith T.,
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Svirskas R., Tector C., Turner R., Ventler E., Wang A.H., Wang X.,
RA	Wang Z.-T., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT	"The genome sequence of Drosophila melanogaster.";
RL	Science 287:2185-2195(2000).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA	Evans C.A., Gocayne J.D., Maniatis P.G., Brandon R.C., Rogers Y.,
RA	Barzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA	Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA	Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Fartin D.,
RA	Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA	Gonzalez M., Houck J., Hoskins R.A., Hoslin D., Howland T.J.,
RA	Ibeagwam C., Jaitani M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA	McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,
RA	Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA	Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA	Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA	Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT	"Sequencing of Drosophila melanogaster genome.";


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Db      187 KTELLQSAIFKSFQEGEVAVPDIEVEFKELIGKEFGVNYKGVMAKKTVAIKKLDSDS 246
OY      268 VTTQAFIDETAVNTKMOHENLVRLVGLYH-OGYIYMEHNSKGNLVNPLRTGRALVNT 326
Db      247 KTAOSLAEASVMTTLQHKLVVLAISFGQDSLTLITCEKGVLEYLTKRRAVITL 306
OY      327 AOLQSLHVAEGMEYLSKRLVHRDLAARNILVSEDLVAKVSPDFGLAKKERGLDSSRL 386
Db      307 EEOGFALDYONGNRYLEEKNIITHRLAANNVLLSDCLAKVSPDFGLAKVDEGLASCKF 366
OY      387 PVKMTAPEALKHGFTSKSVWSFGVLLMEVSTYGRAPYPRMSLKEVSEAVEKGYRMEPP 446
Db      367 PVKMTAPEALELKFSTKSDVWSFGILLMEIFSGRNDYPRDELTLTKIKSNYRMECP 426
OY      447 ECGCPYHVLMSQWEAPARPPFKLAKL 478
Db      427 ECKPFFYQLMKCMADPSRPSFKQLHNEL 458

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RESULT 11

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ID      091X65      PRELIMINARY;      PRT;      509 AA.
AC      091X65;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Similar to lymphocyte-specific protein tyrosine kinase.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Salivary gland;
RA      Strausberg R.;
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      MGD; MGI:96756; Lck.
DR      InterPro: IPR000719; Prot_kinase.
DR      InterPro: IPR000980; SH2.
DR      InterPro: IPR001452; SH3.
DR      InterPro: IPR001245; Tyr_pkinase.
DR      Pfam: PF00069; Pkinase; 1.
DR      Pfam: PF00017; SH2; 1.
DR      PRINTS: PR00401; SH2DOMAIN.
DR      PRINTS: PR00452; SH2DOMAIN.
DR      PRINTS: PR00109; TYRKINASE.
DR      ProDom: PD000001; Prot_kinase; 1.
DR      ProDom: PD000093; SH2; 1.
DR      ProDom: PD000066; SH3; 1.
DR      SMART: SM00252; SH2; 1.
DR      SMART: SM00326; SH3; 1.
DR      SMART: SM00219; TYRK; 1.
DR      PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR      PROSITE: PS50001; SH2; 1.
DR      PROSITE: PS50002; SH3; 1.
KW      ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SQ      SEQUENCE 509 AA; 57942 MW; 3513102F49A/FDOB CRC64;

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Query Match 28.1%; Score 751.5; DB 11; Length 509;

Best Local Similarity 38.3%; Pred. No. 1.8e-52;

Matches 164; Conservative 84; Mismatches 155; Indels 25; Gaps 9;

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OY      65 GELAFKRGDVYITIEACENKSWYRVKHTSGQEGLLAAGLRRERALSADPKLSLMPWFH 124
Db      78 GDLCFEKGEQLRIIE-QSGEMWKAQGLITGQEGFIPFNVAKNSLEPE-----PWFF 129
OY      125 GKISGQANVOQLQPPED-GLFLVRESARHPGDYVLCV-----SFGDVIHYRYLHND-G 176

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Db      130 KNSRDAERKOLLAPGNTHGSLFIRESESTAGSFSLVDFPDQNGEVVYKHYKIRLNDG 189
OY      177 HLTIDEAVFPCNLMOWEHYSKDKGALCTFLVPRKRKHGKSAEELARAGWLLNLOHLYT 236
Db      190 GFYSIRITPPGLHDLVRHTNADSLCTLSRPCQ---TQKQKRWMEDEWVPRFTLK 246
OY      237 LGAOIEGEEFGAVLQGEYIIGQ-KVAVKNIK-CDVTQAFLDETAVNTKMOHENLVRLGV 294
Db      247 LVERLQAGCGEYVWNGYNNCHTAVAVKSLKQGSMSDPAFLAELANKQLOHPALVRLYAV 306
OY      295 ILHOGYIYMEHNSKGNLVNPLFTRGRALVNTAQLQSLHVAEGMEYLSKRLVHRDLA 354
Db      307 VTQEPYITIEYENSGSLVDLFTPGIKLVNKKLLDMAQAIEGMAFLIEQNYIHRDLR 366
OY      355 ARNIVLSEDLVAVSPDFGLAKA-----ERKGLDSSRLPVKMTAPEALKHGFTSKSVWSF 410
Db      367 ANNIVLSDTILSCYADFGARLLEDNEYTAREAKFPKMTAPEALINYGFTTKSDVWSF 426
OY      411 GVLLMEVSTYGRAPYPRMSLKEVSEAVEKGYRMEPPGCPYHVLMSQWEAPARPP 470
Db      427 GILLTEIVTHGRIPYPGMTNPEVIONLERNRGYRVRPDNCPDEELYHLMMLCWKREPRDRPT 486
OY      471 FRKLAKL 478
Db      487 FDYLRVYL 494

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RESULT 12

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ID      093080      PRELIMINARY;      PRT;      526 AA.
AC      093080;
DT      01-NOV-1998 (TREMBLrel. 08, Created)
DT      01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      TSGP1 Src (Fragment).
GN      SRC.
OS      Rous sarcoma virus.
OC      Viruses; Retroviruses; Retroviridae; Alpharetrovirus.
OX      NCBI_Taxid=11886;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92278773; PubMed=1375718;
RA      Moroney A.C., Qureshi S.A., Foster D.A., Brugge J.S.;
RT      Cloning and characterization of a thermostable v-src gene for use in
RT      reversible transformation of mammalian cells.
RL      Oncogene 7:1207-1214(1992).
CC      -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR      EMBL: S37068; AAB96845.1; -.
DR      HSSP: P00524; ISPR.
DR      InterPro: IPR000719; Prot_kinase.
DR      InterPro: IPR000980; SH2.
DR      InterPro: IPR001452; SH3.
DR      InterPro: IPR001245; Tyr_pkinase.
DR      Pfam: PF00069; Pkinase; 1.
DR      Pfam: PF00017; SH2; 1.
DR      Pfam: PF00018; SH3; 1.
DR      PRINTS: PR00401; SH2DOMAIN.
DR      PRINTS: PR00452; SH2DOMAIN.
DR      PRINTS: PR00109; TYRKINASE.
DR      ProDom: PD000001; Prot_kinase; 1.
DR      ProDom: PD000093; SH2; 1.
DR      ProDom: PD000066; SH3; 1.
DR      SMART: SM00252; SH2; 1.
DR      SMART: SM00326; SH3; 1.
DR      SMART: SM00219; TYRK; 1.
DR      PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR      PROSITE: PS50001; SH2; 1.
DR      PROSITE: PS50002; SH3; 1.
KW      ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
FT      NON_TER 526
SQ      SEQUENCE 526 AA; 58970 MW; 2298E6AA3F3D1538 CRC64;

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Db 508 TFEYLQAQL 516

DR ProdOm; PD0000093; SH2; 1.

DR Pfam: PF00017: SH2: 1.

DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TYRKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; SH2DOMAIN.
 DR PROSITE: PS00109; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding: Kinase; SH3 domain; Tyrosine-protein kinase.
 SO SEQUENCE 509 AA; 57946 MW; F1BFE5G237C8BD7E CRC64;

Query Match 27.6%; Score 737.5; DB 6; Length 509;
 Best Local Similarity 37.4%; Pred. No. 2,5e-51;
 Matches 160; Conservative 87; Mismatches 156; Indels 25; Gaps 9;

QY 65 GELAFKGDVVTILEACENKSWRYKHHSTGOGGLLAAGALREALSDPKSLMPFH 124
 DB 78 GDGFCKGQDLRLLE--QSGEMWKAQSLTGGDFIFPNFVAKANSLPE-----PWF 129
 QY 125 KRISGQEAAYQOLPPED--GLFLVRESARHPGDYLCV-----SFGRDYIHYRVLRD-G 176
 DB 130 KNLRSRDAERQLLAPGNTGSLFIRESESTAGSFSLSVNDPQNGEVYKHYKIRMLDNG 189
 QY 177 HLTIIDAVFPCNLMDEVHYSKDKGAICTKLVPRKHKHGTSAEELARAAGLLNQHHT 236
 DB 190 GFYISPRITFPFGHLEHYRYTNASDGLCTRLSRPC---TQPKQPMWEDMEVPRETLK 246
 QY 237 LGAQIEGEGFAGVLOGEYLGO--KVAVKNIK-CDVTAQAFLEDEYAVMTKKQHELVLLGV 294
 DB 247 LVERLGAQGFGEVEMKTYNGHRTKVAVSKLQSGMSMDALAEANLKKOLHOLVLLYAV 306
 QY 295 ILHOGLYIVMEHYSKGNLVNFLTGRALVNTAQLLOFSLHVAEGMEYLESKRLVHRDLA 354
 DB 307 VQEPETIITEYVENSGSLVDLFLKAPSGIKTLTKLIDMAAQIAEGMAFIEERNYIHRDLR 366
 QY 355 ARNIIVSEDLVAKVSPGLAKA----ERKGLDSSRLPVKWTAPALKHGFTSKSVWSF 410
 DB 367 AANILVSDTLSCIAIOGLARLLEDEYTAKEGAKPKIWTAEALNIGFTITKSDVWSF 426
 QY 411 GVLLMEFVSYGRAPKMSLKEVSEAVKGYRMEPEGCPGVHYVLMSSCWEAPARPP 470
 DB 427 GILLTEIYVHGRIPRYGNTNPEYIQLNLENGYRNVPRDNCPELIIQLMLCMKREPRDPT 486
 QY 471 FRKLAERL 478
 DB 487 FDLRSVL 494

RESULT 15

QY 086362 PRELIMINARY; PRT; 545 AA.
 AC 086362;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE PP62V.
 GN SRCIM.
 OS Rous sarcoma virus.
 OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
 NC NCB1_TaxID-11886;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6182936; PubMed=8607264;
 RA Tatarian A., Yatsula B., Shultman M., Molnova E., Kaverina I.,
 Musatkina E., Leskov K., Mizenina O., Zueva E., Calothy G.,
 Dezelee P.;

RT "Two new isoforms of v-src oncogene isolated from low and high
 metastatic RSV-transformed hamster cells.";
 RL Virology 216:347-356(1996).
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: X84074; CA558881.1;-
 DR HSSP: P00524; 1SPR.

DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TYRKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; SH2DOMAIN.
 DR PROSITE: PS00109; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding: Kinase; SH3 domain; Tyrosine-protein kinase.
 SO SEQUENCE 545 AA; 61037 MW; 4CAE34BC75266913 CRC64;

Query Match 27.6%; Score 736; DB 15; Length 545;
 Best Local Similarity 35.6%; Pred. No. 3.7e-51;
 Matches 187; Conservative 82; Mismatches 181; Indels 76; Gaps 16;

QY 14 HCDGSAEELPR-----VSPFLRAWHP-----PVSAMPTRRNAPGT----- 51
 DB 26 HGFAPASQTPNKTAPLTAAPRSR--RPAASORRAAPDHTTPRSF--GIVANPEPLF 81
 QY 52 -----QCITKCEHTRPKPG-----ELAFKRGDVVTILEACENKSWYR 88
 DB 82 GFNTSDVTSPOBARTLAGVTTVALYDESWIETDLSFKKGERLQVNTTEG-NMWL 140
 QY 89 VKNHSGOGGLLAAGALREALSDPKSLMPWHGKTSISGQEAAYQOLPPED--GLFLV 146
 DB 141 AHSVTTGQGYIPSNVAPSDSIOAE-----EMWFGKITRRESRLLNPNPGTFLV 194
 QY 147 RESARHPGYVLCVS-----FGRDYIHYRVLRD-GHLTIIDAVFPCNLMDEVHYSKDK 200
 DB 195 RESSETTKGAYCISVSDPDAKGLNKHYYIRKLDGSGFYITSRQPSLIQVLAAYSKHA 254
 QY 201 GAICTKL--VRPKRHGKTSABEELARAGMLNLQHLTGAQIGEGEGAVLOGEYLQ-Q 257
 DB 255 DGLCHRLTNVCPSTSKPQTGG---LAKDAWEIPRESLRLEVKLGGCGFEGVMGTWNGTT 310
 QY 258 KVAVKNIK-CDVTAQAFLEDEYAVMTKKQHELVRLGLVILHOGLYIVMEHYSKGNLVNLT 316
 DB 311 RVAIKTLKPGTSPFAFLQEAQVMKLRREKLVQYLAAYSEPIYIVLEYSKGLNLFL 370
 QY 317 PTRGRALVNTAQLLOFSLHVAEGMEYLESKRLVHRDLAARNILVSEDLVAKVSPGLAKA 376
 DB 371 KEEMKYLRLPOLVDMAADIAAGMAVVEGMVYHNDLRAANILVGENLECKADGLARL 430
 QY 377 ---ERKGLDSSRLPVKWTAPALKHGFTSKSDVWSFGVLLMEVFSYGRAPYKMSLKE 432
 DB 431 IDNEEYTAQAGAKFPAKWTAPAGLYGRTITKSDVWSFILLTELTKGRVYPPMGNGE 490
 QY 433 VSEAVKGYRMEPEGCPGVHYVLMSSCWEAPARPPRKAERL 478
 DB 491 VLDREVERGYRMPCCPECSLHDLMLCCQWRREBERPTEFYLAQAL 536

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